

QY 61 GACCACTTTGAAATTTTGGAGCCATTTGGGAAAGGCACTTTTGGAAAGGTCTGCAATTGTA 120
Db 61 GACCACTTTGAAATTTTGGAGCCATTTGGGAAAGGCACTTTTGGAAAGGTCTGCAATTGTA 120
QY 121 CAGAGAATGATACCAAGAAGATGTACCAATGAAGTACATGAATACCAAAAGGTGCGTG 180
Db 121 CAGAGAATGATACCAAGAAGATGTACCAATGAAGTACATGAATACCAAAAGGTGCGTG 180
QY 181 GAGGCCAATGAAGTGAAGAAATGTCTTCAAGAACTCCAGATCATCGAGGCTCTGGAGCAC 240
Db 181 GAGGCCAATGAAGTGAAGAAATGTCTTCAAGAACTCCAGATCATCGAGGCTCTGGAGCAC 240
QY 241 CTTTCTCTGGTAAATTTGGTATTTCTTCAAGATGAGGAAGACATTTTCAATGTTGTTG 300
Db 241 CTTTCTCTGGTAAATTTGGTATTTCTTCAAGATGAGGAAGACATTTTCAATGTTGTTG 300
QY 301 GACCTCTCTGGTGGAGACCTGGTTATCACCTGCAACAGAGGTCCACTTCAAGGAA 360
Db 301 GACCTCTCTGGTGGAGACCTGGTTATCACCTGCAACAGAGGTCCACTTCAAGGAA 360
QY 361 GAAACAGTGAAGCTCTTCACTGTGAGCTGGTCTGAGCCCTGGACTACTCTGCAGAACCCAG 420
Db 361 GAAACAGTGAAGCTCTTCACTGTGAGCTGGTCTGAGCCCTGGACTACTCTGCAGAACCCAG 420
QY 421 CGCATCAATTCAGGGATGATGAAGCTGACAAATATTTTACTTGAAGAACATGGGCACGTG 480
Db 421 CGCATCAATTCAGGGATGATGAAGCTGACAAATATTTTACTTGAAGAACATGGGCACGTG 480
QY 481 CACATCAGATTTTCAACATTTCTGCGATGCTGCCAGGAGACACAGATTACCAACATG 540
Db 481 CACATCAGATTTTCAACATTTCTGCGATGCTGCCAGGAGACACAGATTACCAACATG 540
QY 541 GCTGCGACCAAGCCTTACATGCGACCTCGAGATGTTTCACTCCAGAAAAGGAGCGCTAT 600
Db 541 GCTGCGACCAAGCCTTACATGCGACCTCGAGATGTTTCACTCCAGAAAAGGAGCGCTAT 600
QY 601 TCCTTTGCTGTGATCTGTTGCTGCTGGAGTACGGCATATGAATCTCTGAGAGCCGG 660
Db 601 TCCTTTGCTGTGATCTGTTGCTGCTGGAGTACGGCATATGAATCTCTGAGAGCCGG 660
QY 661 AGACCGTATCATATTCGCTCCAGTACTTCCAGCAGGAAATGTTACACACGTTTGAGACG 720
Db 661 AGACCGTATCATATTCGCTCCAGTACTTCCAGCAGGAAATGTTACACACGTTTGAGACG 720
QY 721 ACTGTTGTAACTTACCTTCTGCTGGTCAAGGAAATGGTGCTACTTCTTAAAGGCTA 780
Db 721 ACTGTTGTAACTTACCTTCTGCTGGTCAAGGAAATGGTGCTACTTCTTAAAGGCTA 780
QY 781 CTGGAACCTAATCCAGACCAAGATTTTCTGAGTTATCTGATGTCCAGAACTTCCCGTAT 840
Db 781 CTGGAACCTAATCCAGACCAAGATTTTCTGAGTTATCTGATGTCCAGAACTTCCCGTAT 840
QY 841 ATGAATGATATAAATCTGGATGCACTTTTTCAGAGAGGCTCATTCAGGTTTCAATTCCT 900
Db 841 ATGAATGATATAAATCTGGATGCACTTTTTCAGAGAGGCTCATTCAGGTTTCAATTCCT 900
QY 901 AATAAGGCAGGCTGAAATTTGATCCTTACCTTTTGAATTTGAGAAATGATTTTGAGTCC 960
Db 901 AATAAGGCAGGCTGAAATTTGATCCTTACCTTTTGAATTTGAGAAATGATTTTGAGTCC 960
QY 961 AAACCTCTACATAAGAAAAGGCTGTGGCAAGAAAGAGAGATATGAGGAAATGC 1020
Db 961 AAACCTCTACATAAGAAAAGGCTGTGGCAAGAAAGAGAGATATGAGGAAATGC 1020
QY 1021 GATTCCTCTCAGACATGCTTCTTCAAGAGCACCTTGTCTGTCCAGAGGATTCATA 1080
Db 1021 GATTCCTCTCAGACATGCTTCTTCAAGAGCACCTTGTCTGTCCAGAGGATTCATA 1080
QY 1081 ATTTTCAACAGAGAAAAGTAAACAGGGACTTTTAAACAAAAGACAACTTACGCTTG 1140
Db 1081 ATTTTCAACAGAGAAAAGTAAACAGGGACTTTTAAACAAAAGACAACTTACGCTTG 1140
QY 1141 GAAACAAACCAAGACCCCAAGTGAACAAATGGACAAATGGACACAGGACTCAGTGAGACT 1200

RESULT 2

US-10-620-845-8

; Sequence 8, Application US/10620845

; Publication No. US20040115693A1

; GENERAL INFORMATION:

; APPLICANT: Hu, Yi

; APPLICANT: Nepomnichy, Boris

; APPLICANT: Wang, Xiaoming

; APPLICANT: Donoho, Gregory

; APPLICANT: Scoville, John

; APPLICANT: Walke, D. Wade

; TITLE OF INVENTION: Novel Human Kinase Proteins and Polynucleotides Encoding the Same

; FILE REFERENCE: LEX-0167-USA

; CURRENT APPLICATION NUMBER: US/10/620,845

; CURRENT FILING DATE: 2003-07-15

; PRIOR FILING DATE: 2001-04-24

; PRIOR APPLICATION NUMBER: US 60/199,499

; PRIOR FILING DATE: 2000-04-25

; PRIOR APPLICATION NUMBER: US 60/201,227

; PRIOR FILING DATE: 2000-05-01

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 8

; LENGTH: 1224

; TYPE: DNA

; ORGANISM: homo sapiens

US-10-620-845-8

Query Match 100.0%; Score 1224; DB 17; Length 1224;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAGGCCACACTTCAAGAAACACCACCACTGTTTCATGTAATGAAGATGTCAACTTT 60
Db 1 ATGGAGGCCACACTTCAAGAAACACCACCACTGTTTCATGTAATGAAGATGTCAACTTT 60
QY 61 GACCACCTTGAATTTTTCGAGCCATTGGGAAAGCGAGTTTGGGAAAGGTCTGCAATTGTA 120
Db 61 GACCACCTTGAATTTTTCGAGCCATTGGGAAAGCGAGTTTGGGAAAGGTCTGCAATTGTA 120
QY 121 CAGAAGAATGATACCAAGAAGATGTACGCAATGAAGTACATGAATAAACAAGTGGGTG 180
Db 121 CAGAAGAATGATACCAAGAAGATGTACGCAATGAAGTACATGAATAAACAAGTGGGTG 180
QY 181 GAGCGCAATGAAGTGAAGAAATGTCTTCAAGAACTCCAGATCATCGAGGCTCTGGAGCAC 240
Db 181 GAGCGCAATGAAGTGAAGAAATGTCTTCAAGAACTCCAGATCATCGAGGCTCTGGAGCAC 240
QY 241 CTTTCTCTGGTAAATTTTGTGTTATTCCTTCAAGATGAGGAAAGCATGTTTCATGTTGTTG 300
Db 241 CTTTCTCTGGTAAATTTTGTGTTATTCCTTCAAGATGAGGAAAGCATGTTTCATGTTGTTG 300
QY 301 GACTCTCTGCTGGTGGAGACCTCGGTTATCACTGTAACAGAGGATGTTTCAAGGAA 360
Db 301 GACTCTCTGCTGGTGGAGACCTCGGTTATCACTGTAACAGAGGATGTTTCAAGGAA 360
QY 361 GAAACAGTGAAGCTTCTTCACTGTGAGCTGGTCTGAGCCCTGGACTACTCTGCAGAACCCAG 420
Db 361 GAAACAGTGAAGCTTCTTCACTGTGAGCTGGTCTGAGCCCTGGACTACTCTGCAGAACCCAG 420
QY 421 CGCATCAATTCAGAGGATATGAAGCCTGACAAATATTTTACTTGAAGAACATGGGCACGTG 480
Db 421 CGCATCAATTCAGAGGATATGAAGCCTGACAAATATTTTACTTGAAGAACATGGGCACGTG 480

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Qy 481 CACATCACAGATTTCAACATTGCTGCGATGCTGCCAGGGAGACACAGATTTACCAACATG 540
Db 481 CACATCACAGATTTCAACATTGCTGCGATGCTGCCAGGGAGACACAGATTTACCAACATG 540
Qy 541 GCTGGCACCAGCCTTACATGCGACCTCAGATGTTTCAGCTCCAGAAAAGGAGCAGGCTAT 600
Db 541 GCTGGCACCAGCCTTACATGCGACCTCAGATGTTTCAGCTCCAGAAAAGGAGCAGGCTAT 600
Qy 601 TCCCTTGTGTTGACTGGTGTCTCCTGGAGTACGGCATATGAACCTGCTGAGAGGCCGG 660
Db 601 TCCCTTGTGTTGACTGGTGTCTCCTGGAGTACGGCATATGAACCTGCTGAGAGGCCGG 660
Qy 661 AGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTTGACACAGCTTTGAGACG 720
Db 661 AGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTTGACACAGCTTTGAGACG 720
Qy 721 ACTGTTGTAACTTACCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
Db 721 ACTGTTGTAACTTACCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
Qy 781 CTCGAACCTTAATCCAGACCAACGATTTTCTCAGTATTCAGTATTCAGTATTCAGTATTC 840
Db 781 CTCGAACCTTAATCCAGACCAACGATTTTCTCAGTATTCAGTATTCAGTATTCAGTATTC 840
Qy 841 ATGAATGATATAAAGTGGGATGCGAGTTTTCAGAGAGGCTCATTCAGAGTTTCATTCCT 900
Db 841 ATGAATGATATAAAGTGGGATGCGAGTTTTCAGAGAGGCTCATTCAGAGTTTCATTCCT 900
Qy 901 AATAAGGCGAGCTGAATTTGTGATCTTACCTTTGCAACTTGAAGGAAATGATTTTGGAGTCC 960
Db 901 AATAAGGCGAGCTGAATTTGTGATCTTACCTTTGCAACTTGAAGGAAATGATTTTGGAGTCC 960
Qy 961 AAACCTCTACATAAGAAAAAAGCGTCTGCCAAGAAAGGAGAGGATATGAGGAAATGC 1020
Db 961 AAACCTCTACATAAGAAAAAAGCGTCTGCCAAGAAAGGAGAGGATATGAGGAAATGC 1020
Qy 1021 GATTCCTCTCAGACATGCTCTCTCAAGAGCACCTTGAACCAAGAAAGGAGGAGTTTCATA 1080
Db 1021 GATTCCTCTCAGACATGCTCTCTCAAGAGCACCTTGAACCAAGAAAGGAGGAGTTTCATA 1080
Qy 1081 ATTTTCAACAGAGAAAAAGTAAACAGGACCTTTTAAACAAAGAACCAACCAATCTAGCCTTG 1140
Db 1081 ATTTTCAACAGAGAAAAAGTAAACAGGACCTTTTAAACAAAGAACCAACCAATCTAGCCTTG 1140
Qy 1141 GAAACAAACCAAGACCCCAAGTGAACAAATGGACAAATGGACAAATGGACAAATGGACAA 1200
Db 1141 GAAACAAACCAAGACCCCAAGTGAACAAATGGACAAATGGACAAATGGACAAATGGACAA 1200
Qy 1201 TTTGAGACCTCGAAAGTTTCATA 1224
Db 1201 TTTGAGACCTCGAAAGTTTCATA 1224
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RESULT 3

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US-09-841-683-12
; Sequence 12, Application US/09841683
; Patent No. US20020081600A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Nepomichy, Boris
; APPLICANT: Wang, Xiaoming
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Walke, D. Wade
; TITLE OF INVENTION: No. US20020081600A1el Human Kinase Proteins and Polynucleotides H
; FILE REFERENCE: LEX-0167-USA
; CURRENT APPLICATION NUMBER: US/09/841,683
; CURRENT FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: US 60/199,499
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US 60/201,227
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 12
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 1675
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-841-683-12

Query Match 100.0%; Score 1224; DB 9; Length 1675;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGAGCCCAACACTTCAAGAAAACCAACCAAGTGTGTTGATGAAAAATGAAGATGTCAACTTTT 60
Db 413 ATGGAGCCCAACACTTCAAGAAAACCAACCAAGTGTGTTGATGAAAAATGAAGATGTCAACTTTT 472
Qy 61 GACCACTTTGAAATTTTGGAGCCATTGGGAAAGGCAAGTTTGGGAAAGGCTCTGCAATTGTA 120
Db 473 GACCACTTTGAAATTTTGGAGCCATTGGGAAAGGCAAGTTTGGGAAAGGCTCTGCAATTGTA 532
Qy 121 CAGNAGATGATACCAAGAAAGTGTACGCAATGAAGTACATGAATAACAACAAAGTGGTG 180
Db 533 CAGNAGATGATACCAAGAAAGTGTACGCAATGAAGTACATGAATAACAACAAAGTGGTG 592
Qy 181 GAGCGCAATGAAGTGAAGAAATGCTTCAAGGAACTCCAGATCATGCGAGGCTCTCGAGCAC 240
Db 593 GAGCGCAATGAAGTGAAGAAATGCTTCAAGGAACTCCAGATCATGCGAGGCTCTCGAGCAC 652
Qy 241 CTTTCTCTGTTAATTTTGGTATTCCTTCCAAGATGAGGAAGACATGTTCAATGGTGGTG 300
Db 653 CTTTCTCTGTTAATTTTGGTATTCCTTCCAAGATGAGGAAGACATGTTCAATGGTGGTG 712
Qy 301 GACCTCTCTGTTGGTGGAGACCTGCTGTTATCACCTGCAACAGAACGTCACCTTCAAGGAA 360
Db 713 GACCTCTCTGTTGGTGGAGACCTGCTGTTATCACCTGCAACAGAACGTCACCTTCAAGGAA 772
Qy 361 GAAACAGTGAAGCTCTTTCATCTGTGAGTGTGTCATGCGCCCTGGACTACTCTGCAAGAAC 420
Db 773 GAAACAGTGAAGCTCTTTCATCTGTGAGTGTGTCATGCGCCCTGGACTACTCTGCAAGAAC 832
Qy 421 CGCATCATTCACAGGGATATGAAGCCTTGAACCAATATTTTACTTGACGAACATGGGCACTG 480
Db 833 CGCATCATTCACAGGGATATGAAGCCTTGAACCAATATTTTACTTGACGAACATGGGCACTG 892
Qy 481 CACATCACAGATTTCAACATTGCTGCGATGCTGCCAGGGAGACACAGATTTACCAACATG 540
Db 893 CACATCACAGATTTCAACATTGCTGCGATGCTGCCAGGGAGACACAGATTTACCAACATG 952
Qy 541 GCTGGCACCAGCCTTACATGGCACCTTGAAGTGTTCAGCTCCAGAAAAGGAGCAGGCTAT 600
Db 953 GCTGGCACCAGCCTTACATGGCACCTTGAAGTGTTCAGCTCCAGAAAAGGAGCAGGCTAT 1012
Qy 601 TCCCTTGTGTTGACTGGTGTCTCCTGGAGTACGGCATATGAACCTGCTGAGAGGCCGG 660
Db 1013 TCCCTTGTGTTGACTGGTGTCTCCTGGAGTACGGCATATGAACCTGCTGAGAGGCCGG 1072
Qy 661 AGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTTGACACAGCTTTGAGACG 720
Db 1073 AGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTTGACACAGCTTTGAGACG 1132
Qy 721 ACTGTTGTAACTTACCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
Db 1133 ACTGTTGTAACTTACCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1192
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Db 1193 CTCGAACCTTAATCCAGACCAACGATTTTCTCAGTATTCAGTATTCAGTATTCAGTATTC 1252
Qy 841 ATGAATGATATAAAGTGGGATGCGAGTTTTCAGAGAGGCTCATTCAGAGTTTCATTCCT 900
Db 1253 ATGAATGATATAAAGTGGGATGCGAGTTTTCAGAGAGGCTCATTCAGAGTTTCATTCCT 1312
Qy 901 AATAAGGCGAGCTGAATTTGTGATCTTACCTTTGCAACTTGAAGGAAATGATTTTGGAGTCC 960
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Db 1313 AATAAGGAGGCTGATTTGTGATCCTACCTTTGAACTTGAGAAATGATTTTGGAGTCC 1372
Qy 961 AAACCTCTACATPAGAAAAAAGCGTCTGGCAAAAGAGGAGGATATGAGGAAATGC 1020
Db 1373 AAACCTCTACATPAGAAAAAAGCGTCTGGCAAAAGAGGAGGATATGAGGAAATGC 1432
Qy 1021 GATTTCTTCTACACATGTTCTTCTTCAAGAGACCTTGACTCTGTCTCAGAGAGGATTCATA 1080
Db 1433 GATTTCTTCTACACATGTTCTTCTTCAAGAGACCTTGACTCTGTCTCAGAGAGGATTCATA 1492
Qy 1081 ATTTTCAACAGAGAAAAAGTAAACAGGACTTTTAAACAAAGACCAACCAATCTAGCCCTTG 1140
Db 1493 ATTTTCAACAGAGAAAAAGTAAACAGGACTTTTAAACAAAGACCAACCAATCTAGCCCTTG 1552
Qy 1141 GAAACAAACCAAGACCCCAAGTGAACAAATGGACAAATGGACACAGGACTCAGTGAGACT 1200
Db 1553 GAAACAAACCAAGACCCCAAGTGAACAAATGGACAAATGGACACAGGACTCAGTGAGACT 1612
Qy 1201 TTTTCAGACTCGAAAGTTTCATAA 1224
Db 1613 TTTTCAGACTCGAAAGTTTCATAA 1636

RESULT 4
US-10-620-845-12
; Sequence 12, Application US/10620845
; Publication No. US20040115693A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Nepomnichy, Boris
; APPLICANT: Wang, Xiaoming
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Walke, D. Wade
; TITLE OF INVENTION: Novel Human Kinase Proteins and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0167-USA
; CURRENT APPLICATION NUMBER: US/10/620,845
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US/09/841,683
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: US 60/199,499
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US 60/201,227
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 1675
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-620-845-12

Query Match 100.0%; Score 1224; DB 17; Length 1675;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGAGGCAACACTTCAAGAAAAACCAACAGTGTGTGATGAAATGAGATGTCAACTTT 60
Db 413 ATGGAGGCAACACTTCAAGAAAAACCAACAGTGTGTGATGAAATGAGATGTCAACTTT 472
Qy 61 GACCACCTTGAATTTTGGAGGCAATTTGGGAAAGCGAGTTTGGGAAAGTCTGCATTGTA 120
Db 473 GACCACCTTGAATTTTGGAGGCAATTTGGGAAAGCGAGTTTGGGAAAGTCTGCATTGTA 532
Qy 121 CAGAAGATGATACCAAGAGATGTACGCAATGAAGTACATGAATAAACAAAGTGGGTG 180
Db 533 CAGAAGATGATACCAAGAGATGTACGCAATGAAGTACATGAATAAACAAAGTGGGTG 592
Qy 181 GAGGCAATGAAGTGAGAAATGTCTTCAAGGAACTCCAGATCATCGAGGGTCTGGAGCAC 240
Db 593 GAGGCAATGAAGTGAGAAATGTCTTCAAGGAACTCCAGATCATCGAGGGTCTGGAGCAC 652
Qy 241 CCTTCTCTGTTTAATTTGTGTTTCTTCTTCAAGATGAGGAGACATGTTTCATGTTG 300
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RESULT 5
US-09-841-683-10
; Sequence 10, Application US/09841683
; Patent No. US20020081600A1
; GENERAL INFORMATION:

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Db 713 GACCTCTCTGCTGGGTGAGACCTCGCTTATCACCCTGCAACAGAAAGCTCCACTTCAAGGAA 772
Qy 361 GAAACAGTGAAGCTCTTTCATCTGTGAGTGTGTCTATGCGCCCTGGACTACCTGCAAGAAC 420
Db 773 GAAACAGTGAAGCTCTTTCATCTGTGAGTGTGTCTATGCGCCCTGGACTACCTGCAAGAAC 832
Qy 421 CGCATCATTCACAGGGATATGAAGCCTGACATATTTTACTTGAAGCAACATGGGCAAGTGT 480
Db 833 CGCATCATTCACAGGGATATGAAGCCTGACATATTTTACTTGAAGCAACATGGGCAAGTGT 892
Qy 481 CACATCACAGATTTTCAACATTTGCTGCGATGCTGCCAGGGAGACACAGATTTACCACCATG 540
Db 893 CACATCACAGATTTTCAACATTTGCTGCGATGCTGCCAGGGAGACACAGATTTACCACCATG 952
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Db 953 GCTGGCACCAAGCCTTATACATGGCACCTGAGATGTTTCAGCTCCAGAAAAGGAGCAGGCTAT 1012
Qy 601 TCCTTTGCTGTGACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
Db 1013 TCCTTTGCTGTGACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1072
Qy 661 AGACCGTATCATATTTCCCTCCAGTACTTCCAGCAAGGAAATTTGTACACACATTTTGAGACG 720
Db 1073 AGACCGTATCATATTTCCCTCCAGTACTTCCAGCAAGGAAATTTGTACACACATTTTGAGACG 1132
Qy 721 ACTGTTGTAATTTACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
Db 1133 ACTGTTGTAATTTACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1192
Qy 781 CTGGAACCTTAATCCAGACCAACGATTTTCTCAGTTATCTGATGCTCAGAACTTCCCGTAT 840
Db 1193 CTGGAACCTTAATCCAGACCAACGATTTTCTCAGTTATCTGATGCTCAGAACTTCCCGTAT 1252
Qy 841 ATGAATCATATAAATCTGGGATGAGATTTTTCAGAAAGGCTCATTTCCAGGTTTCATTTCTT 900
Db 1253 ATGAATCATATAAATCTGGGATGAGATTTTTCAGAAAGGCTCATTTCCAGGTTTCATTTCTT 1312
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Db 1313 AATAAGGAGGCTGAAATGTGATCTTACCTTTGAACTTCAGGAAATGATTTTGGAGTCC 1372
Qy 961 AAACCTCTACATAAGAAAAAAGCGCTCTGGCAAAAGAGGAGGATATGAGGAAATGC 1020
Db 1373 AAACCTCTACATAAGAAAAAAGCGCTCTGGCAAAAGAGGAGGATATGAGGAAATGC 1432
Qy 1021 GATTTCTTCTCAGACATGCTTTCTTCAAGAGCACCTTGACTCTGTCCAGAAAGGAGTTCATA 1080
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Qy 1081 ATTTTCAACAGAGAAAAAGTAAACAGGACTTTTAAACAAAGACCAACCAATCTAGCCCTTG 1140
Db 1493 ATTTTCAACAGAGAAAAAGTAAACAGGACTTTTAAACAAAGACCAACCAATCTAGCCCTTG 1552
Qy 1141 GAAACAAACCAAGACCCCAAGTGAACAAATGGACAAATGGACAAATGGACACAGGACTCAGTGAGACT 1200
Db 1553 GAAACAAACCAAGACCCCAAGTGAACAAATGGACAAATGGACAAATGGACACAGGACTCAGTGAGACT 1612
Qy 1201 TTTTCAGACTCGAAAGTTTCATAA 1224
Db 1613 TTTTCAGACTCGAAAGTTTCATAA 1636
```



```
; APPLICANT: Hu, Yi
; APPLICANT: Nepomnichy, Boris
; APPLICANT: Wang, Xiaoming
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Walke, D. Wade
; TITLE OF INVENTION: No. US20020081600A1el Human Kinase Proteins and Polynucleotides H
; FILE REFERENCE: LEX-0167-USA
; CURRENT APPLICATION NUMBER: US/09/841,683
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: US 60/199,499
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US 60/201,227
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-841-683-10

Query Match          95.2%; Score 1165.4; DB 9; Length 1191;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 1172; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 1 ATGGAGGCCAACACCTTCAAGAAAACCCACGAGTGTGATGAAAATGAAGATGTCAACTTT 60
Db 1 ATGGAGGCCAACACCTTCAAGAAAACCCACGAGTGTGATGAAAATGAAGATGTCAACTTT 60
Qy 61 GACCACTTTGAAATTTTGGAGCCATTGGGAAGGCACTTTTGGGAAGGCTCTGCATTGTA 120
Db 61 GACCACTTTGAAATTTTGGAGCCATTGGGAAGGCACTTTTGGGAAGGCTCTGCATTGTA 120
Qy 121 CAGAAGATGATACCAAGAGATGATACCAATGAAGTACATGAATAAACAAGAGTGCCTG 180
Db 121 CAGAAGATGATACCAAGAGATGATACCAATGAAGTACATGAATAAACAAGAGTGCCTG 180
Qy 181 GAGCGCAATGAAGTGAAGAAATGTCTTCAAGAACTCCAGATCATGACGGGTCTGGAGCAC 240
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Db 361 GAAACAGTGAAGCTCTTATCTGTGAGCTGTGTCATGGCCCTGAGTACCTGCAGAACCCAG 420
Qy 421 CGCATCATTACAGGGATGAGGCTGACAAATTTTACTTGAAGAACATGGGACGCTG 480
Db 421 CGCATCATTACAGGGATGAGGCTGACAAATTTTACTTGAAGAACATGGGACGCTG 480
Qy 481 CACATCAGAGATTTCAACATTTCTCGATGCTGCCAGGAGACACAGATTACCAACATG 540
Db 481 CACATCAGAGATTTCAACATTTCTCGATGCTGCCAGGAGACACAGATTACCAACATG 540
Qy 541 GCTGGCACCAGCCTTATCATGTCACCTGAGATGTTTCACTCCAGAAAAGGAGCAGCTAT 600
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Qy 601 TCCCTTGTGTTGATGTTGTTGCTTGGAGTGAAGGATGAACTGCTGAGAGGCCGG 660
Db 601 TCCCTTGTGTTGATGTTGTTGCTTGGAGTGAAGGATGAACTGCTGAGAGGCCGG 660
Qy 661 AGACCGTATCATATTGCTTCCAGTACTTCCAGCAGGAATTTGTACACAGTTTGAAGC 720
Db 661 AGACCGTATCATATTGCTTCCAGTACTTCCAGCAGGAATTTGTACACAGTTTGAAGC 720
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Db 721 ACTGTTCTAACTTACCCCTTCTGCTGCTCAGAGAAATGGTGTCTACCTTCTTAAAGAGTA 780
Qy 781 CTGGAACCTAATCAGACCAACCAAGATTTTCTCAGTTATCTGATGTCCAGAACTTCCCGTAT 840
Db 781 CTGGAACCTAATCAGACCAACCAAGATTTTCTCAGTTATCTGATGTCCAGAACTTCCCGTAT 840
Qy 841 ATGAATGATATAAAGTGGGATGAGTTTTCAGAAAGGCTCATTCAGGTTTCAATTCCT 900
Db 841 ATGAATGATATAAAGTGGGATGAGTTTTCAGAAAGGCTCATTCAGGTTTCAATTCCT 900
Qy 901 AATAAAGCGAGGCTGAATTTGATCTTACCTTTTGAACCTTCAGGAAATGATTTTCGAGTCC 960
Db 901 AATAAAGCGAGGCTGAATTTGATCTTACCTTTTGAACCTTCAGGAAATGATTTTCGAGTCC 960
Qy 961 AAACCTCTACATAGAAAAGAGCGTCTGCAAGAGAGGAGAGGATATGAGGAATGC 1020
Db 961 AAACCTCTACATAGAAAAGAGCGTCTGCAAGAGAGGAGAGGATATGAGGAATGC 1020
Qy 1021 GATTCTCTCAGACATGTTCTTCAAGAGACCTTGAATCTGTCTCAGAGAGGAGTTTCAATA 1080
Db 1021 GATTCTCTCAGACATGTTCTTCAAGAGACCTTGAATCTGTCTCAGAGAGGAGTTTCAATA 1080
Qy 1081 ATTTTCAACAGAGAAAAGTAAACAGGAGCTTTTAAACAAAAGACAAACCAAAATCTAGCCTTG 1140
Db 1081 ATTTTCAACAGAGAAAAGTAAACAGGAGCTTTTAAACAAAAGACAAACCAAAATCTAGCCTTG 1140
Qy 1141 GAACAAACCAAGAACCCACCAAGTGAACAAATGGCAAAATGGACA 1183
Db 1141 GAACAAACCAAGAACCCACCAAGTGAACAAATGGCAAAATGGACA 1183
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RESULT 6

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US-10-620-845-10
; Sequence 10, Application US/10620845
; Publication No. US20040115693A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Nepomnichy, Boris
; APPLICANT: Wang, Xiaoming
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Walke, D. Wade
; TITLE OF INVENTION: Novel Human Kinase Proteins and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0167-USA
; CURRENT APPLICATION NUMBER: US/10/620,845
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US/09/841,683
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: US 60/199,499
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US 60/201,227
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 1191
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-620-845-10
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Query Match          95.2%; Score 1165.4; DB 17; Length 1191;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 1172; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 1 ATGGAGGCCAACACCTTCAAGAAAACCCACGAGTGTGATGAAAATGAAGATGTCAACTTT 60
Db 1 ATGGAGGCCAACACCTTCAAGAAAACCCACGAGTGTGATGAAAATGAAGATGTCAACTTT 60
Qy 61 GACCACTTTGAAATTTTGGAGCCATTGGGAAGGCACTTTTGGGAAGGCTCTGCATTGTA 120
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Db	61	GACCAC	TTTGGAAATTTTCGGAGCCATTTCGGGAAAGCGCAGTTTTCGGGAAAGGCTTCGCA	TTGTA	120
Qy	121	CAGAAGA	TATGATACCAAGAAGATGTACGCAATGAAGTACATGAATAAACAAAGATGCGTG	180	
Db	121	CAGAAGA	TATGATACCAAGAAGATGTACGCAATGAAGTACATGAATAAACAAAGATGCGTG	180	
Qy	181	GAGCGCA	ATGAAGTGAGAAATGTCTTCAAGGAACTCCAGATCATGCAAGGCTCGAGCAC	240	
Db	181	GAGCGCA	ATGAAGTGAGAAATGTCTTCAAGGAACTCCAGATCATGCAAGGCTCGAGCAC	240	
Qy	241	CCTTTC	TCTGGTTAAATTTCTGGTGTATTCCTTCCAAAGATGAGGAAGACATGCTCATGCTGGTGGT	300	
Db	241	CCTTTC	TCTGGTTAAATTTCTGGTGTATTCCTTCCAAAGATGAGGAAGACATGCTCATGCTGGTGGT	300	
Qy	301	GACCTC	TCTGCTGGGTGAGACCTGCGTTATCACTCTGCAACAGAACGTCCTCACTTCAAGGAA	360	
Db	301	GACCTC	TCTGCTGGGTGAGACCTGCGTTATCACTCTGCAACAGAACGTCCTCACTTCAAGGAA	360	
Qy	361	GAACAG	TGAAGCTTTCATCTGTGAGCTGTCTATGCGCCCTGGACTACCTCGAGAACCG	420	
Db	361	GAACAG	TGAAGCTTTCATCTGTGAGCTGTCTATGCGCCCTGGACTACCTCGAGAACCG	420	
Qy	421	CGCATCA	TTCACAGGATGAAGCCTGACAAATATTTTACTTGAAGCAATGCTGGGACAGTG	480	
Db	421	CGCATCA	TTCACAGGATGAAGCCTGACAAATATTTTACTTGAAGCAATGCTGGGACAGTG	480	
Qy	481	CACATCA	CAGATTTTCAACATTTGCTGCGATGTGCTCCAGGGAGACACAGATTAACACCATG	540	
Db	481	CACATCA	CAGATTTTCAACATTTGCTGCGATGTGCTCCAGGGAGACACAGATTAACACCATG	540	
Qy	541	GCTGGC	ACCAGCCCTTACATGGCCACTTGAGATGTTTCAGCTCCAGAAAGAGCAGGCTAT	600	
Db	541	GCTGGC	ACCAGCCCTTACATGGCCACTTGAGATGTTTCAGCTCCAGAAAGAGCAGGCTAT	600	
Qy	601	TCCCTT	GCTGTTGACTGGTGGTCCCTGGGAGTGACGGCATATGAATCTCTGAGAGCCGG	660	
Db	601	TCCCTT	GCTGTTGACTGGTGGTCCCTGGGAGTGACGGCATATGAATCTCTGAGAGCCGG	660	
Qy	661	AGACCG	TATCATATTCGCTCCAGTACTTTCAGCAAGGAAATTTGTACACACGCTTTTGAGACG	720	
Db	661	AGACCG	TATCATATTCGCTCCAGTACTTTCAGCAAGGAAATTTGTACACACGCTTTTGAGACG	720	
Qy	721	ACTGTT	GTGTACTTACCTTTCGCTGGTGCACAGGAAATGGTGTCACTTCTTTAAAAAGCTA	780	
Db	721	ACTGTT	GTGTACTTACCTTTCGCTGGTGCACAGGAAATGGTGTCACTTCTTTAAAAAGCTA	780	
Qy	781	CTCGAA	CCATATCAGACCAACGATTTTCTCAGTTATCTGATGTCAGAACTTCGCGTAT	840	
Db	781	CTCGAA	CCATATCAGACCAACGATTTTCTCAGTTATCTGATGTCAGAACTTCGCGTAT	840	
Qy	841	ATGAAT	TGATATAAACTGGGATGTCAGTTTTCAGAGAGGCTCATTTCCAGGTTTCATTCCT	900	
Db	841	ATGAAT	TGATATAAACTGGGATGTCAGTTTTCAGAGAGGCTCATTTCCAGGTTTCATTCCT	900	
Qy	901	AATAAG	GCGCGCTGAATTTGTGATCTTACCTTTGAACTTGAGGAAATGATTTTGGAGTCC	960	
Db	901	AATAAG	GCGCGCTGAATTTGTGATCTTACCTTTGAACTTGAGGAAATGATTTTGGAGTCC	960	
Qy	961	AAACCT	CTCATATAAGAAAAAGCGTCTGCGAAAGAGGAGAGGATATGAGGAAATGC	1020	
Db	961	AAACCT	CTCATATAAGAAAAAGCGTCTGCGAAAGAGGAGAGGATATGAGGAAATGC	1020	
Qy	1021	GATTC	TTCTCAGACATGCTTCTTTCAGAGCACCTTGACTCTGTCCAGAGGATTCATA	1080	
Db	1021	GATTC	TTCTCAGACATGCTTCTTTCAGAGCACCTTGACTCTGTCCAGAGGATTCATA	1080	
Qy	1081	ATTTTTC	CAACAGAGAAAAAGTAAACAGGACCTTTAAACAAAAACCAACCAAACTTAGACCTTG	1140	
Db	1081	ATTTTTC	CAACAGAGAAAAAGTAAACAGGACCTTTAAACAAAAACCAACCAAACTTAGACCTTG	1140	
Qy	1141	GAA	CAAAACCAAGACCCCAAGTGACAAATGGGACA	1183	
Db	1141	GAA	CAAAACCAAGACCCCAAGTGAGGATGGTCAGAAATAACA	1183	

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RESULT 7
US-10-288-798-44
; Sequence 44, Application US/10288798
; Publication No. US20030207299A1
; GENERAL INFORMATION:
; APPLICANT: BANDMAN, Olga; NGUYEN, Dannie B.;
; APPLICANT: WALIA, Narinder K.; HAPALIA, April J.A.;
; APPLICANT: YAO, Monique G.; GANDHI, Ameena R.;
; APPLICANT: GURURAJAN, Rajagopal; DING, Li;
; APPLICANT: PATTERSON, Chandra; YUE, Henry;
; APPLICANT: BAUGHN, Mariah R.; TRIBOULEY, Catherine M.;
; APPLICANT: THORNTON, Michael; ELLIOTT, Vicki S.;
; APPLICANT: LU, Yan; ISON, Craig H.;
; APPLICANT: AU-YOUNG, Janice; TANG, Y. Tom;
; APPLICANT: AZIMZAI, Yalda; BURRILL, John D.;
; APPLICANT: MARCUS, Gregory A.; ZINGLER, Kurt A.;
; APPLICANT: LU, Dyung Aina M.; LAL, Preeti G.;
; APPLICANT: RAMKUMAR, Javalaxmi; WARREN, Bridget A.;
; APPLICANT: KEARNEY, Liam; POLICKY, Jennifer L.;
; APPLICANT: THANGAVELU, Kavitha; BURFORD, Neil;
; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCE: PI-0209 USA
; CURRENT APPLICATION NUMBER: US/10/288,798
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: PCT/US01/27219
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/240,542
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US 60/238,389
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 60/236,499
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 60/234,902
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US 60/232,654
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US 60/231,357
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: US 60/229,873
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PERL Program
; SEQ ID NO 44
; LENGTH: 1594
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030207299A1 7946584CBI
US-10-288-798-44

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241 CCTTCTCGTGAATTTGTTGTTATTCCTTCAAGATGAGGAGCATGTTTCATGTTGTTG 300
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
644 CCTTCTCGTGAATTTGTTGTTATTCCTTCAAGATGAGGAGCATGTTTCATGTTGTTG 703
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
301 GACCTCTCGTGGTGGAGACCTCGTTATCACCTGCAACAGAGCTCCACTTCAAGGAA 360
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
704 GACCTCTCGTGGTGGAGACCTCGTTATCACCTGCAACAGAGCTCCACTTCAAGGAA 763
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
361 GAAACAGTGAAGCTCTTTCATCTGTGAGCTGTGCTGATGGCCCTGGACTACCTTCAGAACG 420
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
764 GAAACAGTGAAGCTCTTTCATCTGTGAGCTGTGCTGATGGCCCTGGACTACCTTCAGAACG 823
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
421 CGCATCTTACAGGAGTATGAAGCTGACAAATATTTTACTTGGAGCAATGCGACCTG 480
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
824 CGCATCTTACAGGAGTATGAAGCTGACAAATATTTTACTTGGAGCAATGCGACCTG 883
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
481 CACATCAGAGTTTCAACATTTGCTGCGATGCTGCCAGGGAGACACAGATTACCAACATG 540
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
884 CACATCAGAGTTTCAACATTTGCTGCGATGCTGCCAGGGAGACACAGATTACCAACATG 943
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
541 GCTGGACCAAGCTTACATGGCAGCTGAGATGTTTCAGCTCCAGAAAGGAGCGGCTAT 600
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
944 GCTGGACCAAGCTTACATGGCAGCTGAGATGTTTCAGCTCCAGAAAGGAGCGGCTAT 1003
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
601 TCCTTTGCTGTTGACTGTGTGCTCGGAGTGCAGCATATGAATCTGCTGAGAGCGCG 660
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1004 TCCTTTGCTGTTGACTGTGTGCTCGGAGTGCAGCATATGAATCTGCTGAGAGCGCG 1063
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
661 AGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATGTACACACGTTTGAAGCG 720
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1064 AGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATGTACACACGTTTGAAGCG 1123
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
721 ACTGTTGTAATTTACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1124 ACTGTTGTAATTTACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1183
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1184 CTGGAACCTAATCAGACCAAGCTTTTCTCAGTTATCTGATGTCAGAACTTCCCGTAT 1243
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
841 ATGAATGATATAAATCGGATGCAAGTTTTCAGAGAGGCTCATTCAGAGTTTTCATTCCT 900
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1244 ATGAATGATATAAATCGGATGCAAGTTTTCAGAGAGGCTCATTCAGAGTTTTCATTCCT 1303
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
901 AATAAGCAGGCTGAATTTGATGCTTACCTTTGAACTTGAGGAAATGATTTTGGAGTCC 960
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1304 AATAAGCAGGCTGAATTTGATGCTTACCTTTGAACTTTGAGGAAATGATTTTGGAGTCC 1363
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
961 AAACCTCTACATAAGAAAAAAGCGTCTGCAAGAGGAGGAGGATATGAGGAAATGC 1020
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1364 AAACCTCTACATAAGAAAAAAGCGTCTGCAAGAGGAGGAGGATATGAGGAAATGC 1423
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1021 GATTTCTCTCAGACATGCTTTCTTCAAGAGCACCTTTGACTCTGTCCAGAGGAGTTCATA 1080
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1424 GATTTCTCTCAGACATGCTTTCTTCAAGAGCACCTTTGACTCTGTCCAGAGGAGTTCATA 1483
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1081 ATTTTCAACAGAGAAAAAGTAAACAGGAGCTTTTAAACAAAAGAACCAAAATCTAGCCTTG 1140
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1484 ATTTTCAACAGAGAAAAAGTAAACAGGAGCTTTTAAACAAAAGAACCAAAATCTAGCCTTG 1543
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1141 GAACAAACCAAGACCCACAGAGTACAAATGACAAATGGACA 1183
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1544 GAACAAACCAAGACCCCAAGGAGGAGGATGGTCAGAAATAACA 1586

RESULT 8

US-10-362-892-44

; Sequence 44, Application US/10362892

; Publication No. US20040038881A1

; GENERAL INFORMATION:

; APPLICANT: INCYTE GENOMICS, INC.; BANDMAN, Olga

; APPLICANT: NGUYEN, Daniel B.; WALIA, Narinder K.

; APPLICANT: HAFALIA, April J.A.; YAO, Monique G.

APPLICANT: GANDHI, Ameena R.; GURURAJAN, Rajagopal
APPLICANT: DING, Li; PATTERSON, Chandra S.
APPLICANT: YUE, Henry; BAUGHN, Mariah R.
APPLICANT: TRIBOULEY, Catherine M.; THORNTON, Michael B.
APPLICANT: ELLIOTT, Vicki S.; LU, Yan
APPLICANT: ISON, Craig H.; AU-YOUNG, Janice K.
APPLICANT: TANG, Y. Tom; AZIMZAI, Yalda
APPLICANT: BURRILL, John D.; MARCUS, Gregory A.
APPLICANT: ZINGLER, Kurt A.; LU, Dyung Aina M.
APPLICANT: LAU, Preeti G.; RAMKUMAR, Jayalaxmi
APPLICANT: WARREN, Bridget A.; KEARNEY, Liam
APPLICANT: POLICKY, Jennifer L.; THANGAVELU, Kavitha
TITLE OF INVENTION: HUMAN KINASES
FILE REFERENCE: PF-0209 USN
CURRENT APPLICATION NUMBER: US/10/362,892
CURRENT FILING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: PCT/US01/27219
PRIOR FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 60/229,873
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: US 60/231,357
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: US 60/232,654
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: US 60/234,902
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: US 60/236,499
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: US 60/238,389
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: US 60/240,542
PRIOR FILING DATE: 2000-10-13
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PERL Program
SEQ ID NO 44
LENGTH: 1594
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20040038881A1 7946584CB1
US-10-362-892-44

Query Match 95.2%; Score 1165.4; DB 16; Length 1594;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 1172; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 1 ATGGAGCCCAACCTTCAAGAAACCCACCATGTTTCATGAAATGAAGATGTCAACTTT 60
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
404 ATGGAGCCCAACCTTCAAGAAACCCACCATGTTTCATGAAATGAAGATGTCAACTTT 463
Qy 61 GACCACCTTTGAAATTTTCGAGCCATTTGGGAAAGCGAGTTTGGGAAAGGTCTGCAATTGA 120
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
464 GACCACCTTTGAAATTTTCGAGCCATTTGGGAAAGCGAGTTTGGGAAAGGTCTGCAATTGA 523
Qy 121 CAGAAGAAATGATACCAAGAGAGTGTACGCAATGAAGTACATGAATAAACAAGAGTGGTG 180
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
524 CAGAAGAAATGATACCAAGAGAGTGTACGCAATGAAGTACATGAATAAACAAGAGTGGTG 583
Qy 181 GAGCGCAATGAGTGAGAAATGCTTCAAGGAACCTCCAGATCATGCGGGTCTCGAGCAC 240
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
584 GAGCGCAATGAGTGAGAAATGCTTCAAGGAACCTCCAGATCATGCGGGTCTCGAGCAC 643
Qy 241 CCTTTCCTGGTTAATTTTGTGTATTCTTCAAGATGAGGAAGACATGTTTCATGTTGTTG 300
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644 CCTTTCCTGGTTAATTTTGTGTATTCTTCAAGATGAGGAAGACATGTTTCATGTTGTTG 703
Qy 301 GACTCTCTGCTGGGTGAGACCTGCGTTATCACCTGCAACAGAGCGTCCACTTCAAGGAA 360
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
704 GACTCTCTGCTGGGTGAGACCTGCGTTATCACCTGCAACAGAGCGTCCACTTCAAGGAA 763
Qy 361 GAAACAGTGAAGCTCTTTCATCTGTGAGCTGTGCTGATGGCCCTGGACTACCTTCAGAACG 420

Db 764 GAAACAGTGAAGCTCTTCACTCTGTGAGCTGGTCTATGGCCCTGGACTCCTCGAGAACCCAG 823
Qy 421 CGCATCATTCACAGGATATGAAGCTGACAAATATTTACTTGGACGAACATGGGACGCTG 480
Db 824 CGCATCATTCACAGGATATGAAGCTGACAAATATTTACTTGGACGAACATGGGACGCTG 883
Qy 481 CACATCACAGATTTCAACATTTCTGCGATGCTGCCAGGAGACACAGATTTACCAACCATG 540
Db 884 CACATCACAGATTTCAACATTTCTGCGATGCTGCCAGGAGACACAGATTTACCAACCATG 943
Qy 541 GCTGGCACCAGCCTTACATGCACTGAGATGTTTCAGCTCAGAAAAGGAGCAGGCTAT 600
Db 944 GCTGGCACCAGCCTTACATGCACTGAGATGTTTCAGCTCAGAAAAGGAGCAGGCTAT 1003
Qy 601 TCCTTTGCTGTTGACTGCTGGTGGTCCCTGGGAGTGACGGCATATGAACCTGTCAGAGCCCG 660
Db 1004 TCCTTTGCTGTTGACTGCTGGTGGTCCCTGGGAGTGACGGCATATGAACCTGTCAGAGCCCG 1063
Qy 661 AGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTTGTACACACGTTTGGAGCG 720
Db 1064 AGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTTGTACACACGTTTGGAGCG 1123
Qy 721 ACTGTTGTAACCTTACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
Db 1124 ACTGTTGTAACCTTACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1183
Qy 781 CTCGAACTTAATCCAGACCAACGATTTCTGAGTATCTGATGTCAGAACTTCCGCTAT 840
Db 1184 CTCGAACTTAATCCAGACCAACGATTTCTGAGTATCTGATGTCAGAACTTCCGCTAT 1243
Qy 841 ATGAATGATATAAATCGGATGACGATTTTTCAGAAAGGCTCATTCAGGTTTCAATTCCT 900
Db 1244 ATGAATGATATAAATCGGATGACGATTTTTCAGAAAGGCTCATTCAGGTTTCAATTCCT 1303
Qy 901 AATAAGGAGGCTGAATTTGATGCTTACCTTTGAACTTGAGGAATGATTTGGAGTCC 960
Db 1304 AATAAGGAGGCTGAATTTGATGCTTACCTTTGAACTTGAGGAATGATTTGGAGTCC 1363
Qy 961 AATCTCTACATAAGAAAAAAGGCTCTGGCAAGAGGAGGAGATGAGGAATGC 1020
Db 1364 AATCTCTACATAAGAAAAAAGGCTCTGGCAAGAGGAGGAGATGAGGAATGC 1423
Qy 1021 GATCTCTCAGACATGCTTCTTCAAGAGCAGCTTGTCTGTCCAGAGGAGTTTCATA 1080
Db 1424 GATCTCTCAGACATGCTTCTTCAAGAGCAGCTTGTCTGTCCAGAGGAGTTTCATA 1483
Qy 1081 ATTTTCACAGAGAAAGTAAACAGGAGCTTTTAAACAGAACCAACCAATCTAGCCTTG 1140
Db 1484 ATTTTCACAGAGAAAGTAAACAGGAGCTTTTAAACAGAACCAACCAATCTAGCCTTG 1543
Qy 1141 GAAACAAACCAAGACCCCAAGTGAACAAATGGACAAATGGACA 1183
Db 1544 GAACAAACCAAGACCCCAAGTGAACAAATGGACAAATGGACA 1586

RESULT 9
US-10-182-243-1
; Sequence 1, Application US/10182243
; Publication No. US20040048310A1
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY D.
; APPLICANT: WHYTE, DAVID
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAM, SUCHA
; APPLICANT: MARTINEZ, RICARDO
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES AND PROTEIN KINASE-LIKE
; TITLE OF INVENTION: ENZYMES
; FILE REFERENCE: 038602/1366
; CURRENT APPLICATION NUMBER: US/10/182,243
; CURRENT FILING DATE: 2003-07-07
; PRIOR APPLICATION NUMBER: PCT/US01/02337
; PRIOR FILING DATE: 2001-01-25

; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1594
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-182-243-1
Query Match 95.2%; Score 1165.4; DB 16; Length 1594;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 1172; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
Qy 1 ATGGAGCCACACTTCAAGAAAAACCAACAGTGTGTTGATGAAAAATGAAGATGTCAACTTT 60
Db 404 ATGGAGCCACACTTCAAGAAAAACCAACAGTGTGTTGATGAAAAATGAAGATGTCAACTTT 463
Qy 61 GACCACCTTGAATTTTGGAGCCATTTGGGAAAGGCGAGTTTGGGAAAGGCTCTGCAATTGTA 120
Db 464 GACCACCTTGAATTTTGGAGCCATTTGGGAAAGGCGAGTTTGGGAAAGGCTCTGCAATTGTA 523
Qy 121 CAGAAAGATGATACCAAGAAAGATGTCGCAATGAAGTACATGAATAAACAAGCTGCGTG 180
Db 524 CAGAAAGATGATACCAAGAAAGATGTCGCAATGAAGTACATGAATAAACAAGCTGCGTG 583
Qy 181 GAGCGCAATGAAGTGAAGAAATGCTTCAAGAACTCCAGATCATGCAAGGCTCTGGAGCAC 240
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Qy 241 CCTTTCCTGGTAAATTTTGGTATTTCTTCCAGATGAGGAAGACATGTTTCATGGTGGTG 300
Db 644 CCTTTCCTGGTAAATTTTGGTATTTCTTCCAGATGAGGAAGACATGTTTCATGGTGGTG 703
Qy 301 GACCTCTGCTGGTGGAGACCTGCGTTTATCCTGCAACAGAACGCTCCACTTCAAGGAA 360
Db 704 GACCTCTGCTGGTGGAGACCTGCGTTTATCCTGCAACAGAACGCTCCACTTCAAGGAA 763
Qy 361 GAAACAGTGAAGCTTTCATCTGTGAGCTGGTATGCGCCCTGGACTACCTGCAAGAACAG 420
Db 764 GAAACAGTGAAGCTTTCATCTGTGAGCTGGTATGCGCCCTGGACTACCTGCAAGAACAG 823
Qy 421 CGCATCATTCACAGGATATGAAGCTTGAAGCTTGAACAAATATTTACTTGCAGCAACATGGGCA 480
Db 824 CGCATCATTCACAGGATATGAAGCTTGAAGCTTGAACAAATATTTACTTGCAGCAACATGGGCA 883
Qy 481 CACATCACAGATTTCAACATTTCTGCGATGCTGCCAGGAGACACAGATTTACCAACCATG 540
Db 884 CACATCACAGATTTCAACATTTCTGCGATGCTGCCAGGAGACACAGATTTACCAACCATG 943
Qy 541 GCTGGCACCAGCCTTACATGCACTGAGATGTTTCAGCTCCAGAAAAGGAGCAGGCTAT 600
Db 944 GCTGGCACCAGCCTTACATGCACTGAGATGTTTCAGCTCCAGAAAAGGAGCAGGCTAT 1003
Qy 601 TCCTTTGCTGTTGACTGCTGGTGGTCCCTGGGAGTGACGGCATATGAACCTGTCAGAGCCCG 660
Db 1004 TCCTTTGCTGTTGACTGCTGGTGGTCCCTGGGAGTGACGGCATATGAACCTGTCAGAGCCCG 1063
Qy 661 AGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTTGTACACACGTTTGGAGCG 720
Db 1064 AGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTTGTACACACGTTTGGAGCG 1123
Qy 721 ACTGTTGTAACCTTACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
Db 1124 ACTGTTGTAACCTTACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1183
Qy 781 CTGGAACCTAATCCAGACCAACGATTTTCTCAGTTATCTGATGTCAGAACTTCCGCTAT 840
Db 1184 CTGGAACCTAATCCAGACCAACGATTTTCTCAGTTATCTGATGTCAGAACTTCCGCTAT 1243
Qy 841 ATGAATGATATAAATCGGATGACGATTTTTCAGAAAGGCTCATTCAGGTTTCAATTCCT 900
Db 1244 ATGAATGATATAAATCGGATGACGATTTTTCAGAAAGGCTCATTCAGGTTTCAATTCCT 1303
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Db 1304 AATAAGGCGAGCTGAATGTGATCTTACCTTTGAACTTGAAGGAATGATTTGGAGTCC 1363
Qy 961 AAACCTCTACATAAGAAAAAAGCGTCTGCAAGAGGAGGAGGATATGAGGAAATGC 1020
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Db 1484 ATTTTCAACAGAGAAAAAGTAAACAGGACCTTTTAAACAAAGACCAACCAATCTAGCCTTG 1543
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Db 1544 GAAACCAACCAAGACCCCAAGTGAACAAATGGACAAATGGACA 1586

RESULT 10

US-10-410-764-102
; Sequence 102, Application US/10410764
; Publication No. US20040005664A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Weich, Nadine S.
; APPLICANT: Olandt, Peter J.
; APPLICANT: Tsai, Fong-Ying
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Carroll, Joseph M.
; TITLE OF INVENTION: 26199, 33530, 33949, 47148, 50226,
; TITLE OF INVENTION: 58764, 62113, 32144, 32235, 23565, 13305, 14911, 86216,
; TITLE OF INVENTION: 25206 AND 8843 MOLECULES AND USES THEREFOR
; FILE REFERENCE: MPI03-0520MNM
; CURRENT APPLICATION NUMBER: US/10/410,764
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: US 09/924,358
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/229,300
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: US 10/350,553
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: US 60/351,572
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: US 09/966,614
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US 60/238,054
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: US 10/281,094
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 60/347,815
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 10/076,535
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/269,440
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102
; LENGTH: 1191
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)....(1191)
US-10-410-764-102

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Best Local Similarity 99.0%; Pred. No. 0;
Matches 1171; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
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Db 1 ATGGAGCCCAACTCTCAAGAAACACCAAGTGTTCATGAAATGAAGATGTCAACTTT 60
Qy 61 GACCACCTTGAATTTTGGAGCCATTTGGGAAAGGCGAGTTTGGGAAAGGCTGCAATTGTA 120
Db 61 GACCACCTTGAATTTTGGAGCCATTTGGGAAAGGCGAGTTTGGGAAAGGCTGCAATTGTA 120
Qy 121 CAGAAGAATGATACCAAGAAAGATGTAGCAATGAAGTACATGAATAAACAAGTGGCTG 180
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Qy 181 GAGCGCAATGAAGTGAAGAAATGTCTTCAAGAACTCCAGATCATGCGAGGCTCTGGAGCAC 240
Db 181 GAGCGCAATGAAGTGAAGAAATGTCTTCAAGAACTCCAGATCATGCGAGGCTCTGGAGCAC 240
Qy 241 CCTTCTCTGTTAATTTTGGTATTTCTTCCAGATGAGGAAGACATGTTTCATGGTGTG 300
Db 241 CCTTCTCTGTTAATTTTGGTATTTCTTCCAGATGAGGAAGACATGTTTCATGGTGTG 300
Qy 301 GACCTCTCTGTTGGTGGAGACCTGCGTTATCACCTGCAACAGAACTCCACTTCAAGGAA 360
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Qy 361 GAAACAGTGAAGCTCTTTCATCTGTGAGCTGGTCAAGCCCTGGAGTACCTTCGAGAAC 420
Db 361 GAAACAGTGAAGCTCTTTCATCTGTGAGCTGGTCAAGCCCTGGAGTACCTTCGAGAAC 420
Qy 421 CGCATCATTCACAGGATATGAAGCCCTGACATATTTTACTTGAAGAACATGCGCACGTG 480
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Db 481 CACATCAGATTTTCAACATTTGCTGCGATGCTGCCAGGAGGAGACAGATATACCAACATG 540
Qy 541 GCTGGCACCAGCCCTTACATGGCACCTGAGATGTTTCAGCTCCAGAAAGGAGGAGCTAT 600
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Qy 601 TCCCTTGTGTTGATGCTGGTGGTCCCTGGAGTGAAGGATATGAAGTGTGAGAGGCGG 660
Db 601 TCCCTTGTGTTGATGCTGGTGGTCCCTGGAGTGAAGGATATGAAGTGTGAGAGGCGG 660
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Db 661 AGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTTGTACACACCTTTGAGACG 720
Qy 721 ACTGTGTAACTTACCCCTTCTGCTGGTCAAGGAAATGGTGTCACTTCTTAAAGGCTA 780
Db 721 ACTGTGTAACTTACCCCTTCTGCTGGTCAAGGAAATGGTGTCACTTCTTAAAGGCTA 780
Qy 781 CTCGAACTTAATCAGACCAACGATTTTCTCAGTATATCTGATGTCCGAACTTCCCGTAT 840
Db 781 CTCGAACTTAATCAGACCAACGATTTTCTCAGTATATCTGATGTCCGAACTTCCCGTAT 840
Qy 841 ATGAATGATATAAACTGGGATGCGAGTTTTCAGAAAGGAGGCTCATTTCCAGGTTTCACT 900
Db 841 ATGAATGATATAAACTGGGATGCGAGTTTTCAGAAAGGAGGCTCATTTCCAGGTTTCACT 900
Qy 901 AATAAAGCGAGCTGAATTTGTGATCTCTACCTTTTGAAGTGAAGGAAATGATTTTGGAGTCC 960
Db 901 AATAAAGCGAGCTGAATTTGTGATCTCTACCTTTTGAAGTGAAGGAAATGATTTTGGAGTCC 960
Qy 961 AAACCTCTACATAAGAAAAAAGCGTCTGCAAGAGGAGGAGGATATGAGGAAATGC 1020
Db 961 AAACCTCTACATAAGAAAAAAGCGTCTGCAAGAGGAGGAGGATATGAGGAAATGC 1020
Qy 1021 GATTCTCTCAGACATGCTCTTCTTCAAGAGCACCTTGTACTCTGCTCCAGAGGAGTTCATA 1080


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Db 183 GAGCGCAATGAAGTGAAGATGCTTCAAGGAACCTCAGATCATGCGGGTCTGGAGCAC 242
Qy 241 CTTTCTCTGGTAAATTTGGTATCTCTCCAGATGAGGAGACATGTTCAATGGTGTG 300
Db 243 CTTTCTCTGGTAAATTTGGTATCTCTCCAGATGAGGAGACATGTTCAATGGTGTG 302
Qy 301 GACCTCTCTGGTGGAGACCTGGGTATACCTGCAACAGAGCTCCACATTCAGGAA 360
Db 303 GACCTCTCTGGTGGAGACCTGGGTATACCTGCAACAGAGCTCCACATTCAGGAA 362
Qy 361 GAAACAGTGAAGCTCTTCACTGTGAGCTGTGATGCGCTGCACTCTGCAAGACCA 420
Db 363 GAAACAGTGAAGCTCTTCACTGTGAGCTGTGATGCGCTGCACTCTGCAAGACCA 422
Qy 421 CCATCATTCACAGGATATGAAGCTGACATATTTACTTGCAACATGGGACCTG 480
Db 423 CCATCATTCACAGGATATGAAGCTGACATATTTACTTGCAACATGGGACCTG 482
Qy 481 CACATCAGAGATTTCAACATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
Db 483 CACATCAGAGATTTCAACATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 542
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Db 543 GCTGGACCAAGCTTTACATGCACTGAGATGTTTCACTTCAGAAAAGGAGGAGCTAT 602
Qy 601 TCTTTTGTCTGTTGACTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
Db 603 TCTTTTGTCTGTTGACTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 662
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Qy 721 ACTGTTGTAACTTACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
Db 723 ACTGTTGTAACTTACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 782
Qy 781 CTCGAACTTATCCAGACCAAGATTTTCTCAGTTATCTGATGCTGCTGCTGCTGCTG 840
Db 783 CTCGAACTTATCCAGACCAAGATTTTCTCAGTTATCTGATGCTGCTGCTGCTGCTG 842
Qy 841 ATGAATGATATAAATCGGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
Db 843 ATGAATGATATAAATCGGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 902
Qy 901 AATAAGGCGGCTGAATTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
Db 903 AATAAGGCGGCTGAATTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 962
Qy 961 AAACCTCTACATAAGAAAAAAGGCTGCTGCAAGAGGAGGAGATATCAGGAAATGC 1020
Db 963 AAACCTCTACATAAGAAAAAAGGCTGCTGCAAGAGGAGGAGATATCAGGAAATGC 1022
Qy 1021 GATTTCTCTCAGACATGCTTTCTTCAAGACGACCTTGTCTGCTGCTGCTGCTGCTGCT 1080
Db 1023 GATTTCTCTCAGACATGCTTTCTTCAAGACGACCTTGTCTGCTGCTGCTGCTGCTGCT 1082
Qy 1081 ATTTTCAACAGGAAAGTAAACAGGACCTTTTAAACAAACACACCAAAATCTAGCCTTG 1140
Db 1083 ATTTTCAACAGGAAAGTAAACAGGACCTTTTAAACAAACACACCAAAATCTAGCCTTG 1142
Qy 1141 GAAACAAACCAAGACCCCAAGTGAACATTTGCAAAATGGACCA 1183
Db 1143 GAAACAAACCAAGACCCCAAGTGAACATTTGCAAAATGAACA 1185
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RESULT 14

US-10-667-442-1

; Sequence 1, Application US/10667442

; Publication No. US20040043466A1

; GENERAL INFORMATION:

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; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001160DIV II
; CURRENT APPLICATION NUMBER: US/10/667,442
; CURRENT FILING DATE: 2003-09-23
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1485
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-667-442-1
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Query Match 94.8%; Score 1160.6; DB 16; Length 1485;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 1169; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

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Db 3 ATGGGAGCCACACTTCAAGAAAAACCAACCAAGTGTTCATGAAAAATGAAGATGTCAACTTT 62
Qy 61 GACCACTTTGAAATTTTTCGAGCCATTGGGAAAGGCGAGTTTGGGAAAGGTCTGCAATTTGA 120
Db 63 GACCACTTTGAAATTTTTCGAGCCATTGGGAAAGGCGAGTTTGGGAAAGGTCTGCAATTTGA 122
Qy 121 CAGNAGATGATACCAAGAGATGTAGCAATGAGTACATGATTAACAAGAGTGGCTG 180
Db 123 CAGAAGATGATACCAAGAGATGTGGCAATGAGTACATGATTAACAAGAGTGGCTG 182
Qy 181 GAGCGCAATCAAGTGAAGAAATGCTTCAAGAACTCCAGAACTCATGAGGCTCTGGAGCAC 240
Db 183 GAGCGCAATCAAGTGAAGAAATGCTTCAAGAACTCCAGAACTCATGAGGCTCTGGAGCAC 242
Qy 241 CTTTCTCTGTTAATTTTGGTATTCCTTCAAGATGAGGAAAGCATGTTTCAATGGTGTG 300
Db 243 CTTTCTCTGTTAATTTTGGTATTCCTTCAAGATGAGGAAAGCATGTTTCAATGGTGTG 302
Qy 301 GACCTCTCTGTTGAGGAGACCTGCGTTATCCTGCAAGTCAAGACGTCACATTCAGGAA 360
Db 303 GACCTCTCTGTTGAGGAGACCTGCGTTATCCTGCAAGTCAAGACGTCACATTCAGGAA 362
Qy 361 GAAACAGTGAAGCTCTTTCATCTGTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
Db 363 GAAACAGTGAAGCTCTTTCATCTGTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 422
Qy 421 CGCATCATTCACAGGATATGAAGCTGCAATATTTTACTTGAACAAATGGGACAGTG 480
Db 423 CGCATCATTCACAGGATATGAAGCTGCAATATTTTACTTGAACAAATGGGACAGTG 482
Qy 481 CACATCAGATTTCAACATTTGCTGCGATGCTGCCAGGAGACACAGATTTACCAACCATG 540
Db 483 CACATCAGATTTCAACATTTGCTGCGATGCTGCCAGGAGACACAGATTTACCAACCATG 542
Qy 541 GCTGGACCAAGCTTTTACATGCACTGAGATGTTTCACTGCTCCAGAAAAGGAGGAGCTAT 600
Db 543 GCTGGACCAAGCTTTTACATGCACTGAGATGTTTCACTGCTCCAGAAAAGGAGGAGCTAT 602
Qy 601 TCTTTGCTGTTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
Db 603 TCTTTGCTGTTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 662
Qy 661 AGACGCTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTTGTACACAGCTTTGAGACG 720
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Qy 721 ACTGTTGTAACTTACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
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Qy 781 CTGAACTTATCCAGACCAAGATTTTCTCAGTTATCTGATGCTGCTGCTGCTGCTGCTG 840
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Db 783 CTCGAACCTAATCCAGACCAACGATTTTCTCAGTTATCTGATGTCCAGAACTTCCCGTAT 842
Qy 841 ATGAATGATATAAAGCTGGGATGAGTTTTCAGAGAGGCTCATTCAGGTTTCATTCCT 900
Db 843 ATGAATGATATAAAGCTGGGATGAGTTTTCAGAGAGGCTCATTCAGGTTTCATTCCT 902
Qy 901 AATAAGGCGAGGCTGAATTTGATGCTTACCTTTGAACTTCAGGAAATGATTTTGGAGTCC 960
Db 903 AATAAGGCGAGGCTGAATTTGATGCTTACCTTTGAACTTCAGGAAATGATTTTGGAGTCC 962
Qy 961 AAAACCTCTACATTAAGAAAAAAGCGCTCGGCAAGAGAGAGGATATGAGGAAATGC 1020
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Qy 1081 ATTTTCAACAGAGAAAAAGTAAACAGGGACTTTTAAACAAAAGACAAACCAAAATCTAGCCTTG 1140
Db 1083 ATTTTCAACAGAGAAAAAGTAAACAGGGACTTTTAAACAAAAGACAAACCAAAATCTAGCCTTG 1142
Qy 1141 GAACAAACCAAGACCCACCAAGTGACAAATGGACAAATGGACA 1183
Db 1143 GAACAAACCAAGACCCACCAAGTGAGGATGGTCAGAAATAACA 1185

RESULT 15
US-10-108-260A-231
; Sequence 231, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 231
; LENGTH: 2063
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-108-260A-231

Query Match 84.3%; Score 1032.2; DB 16; Length 2063;
Best Local Similarity 99.7%; Pred. No. 3.3e-301;
Matches 1034; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 334 ATGGGAGCCAACTTCAAGAAAAACCAAGTGTTCATGATAAATGAAGATGTCAACTTT 393
Qy 61 GACCACCTTCAAAATTTTGGCGAGCCATTGGGAAAGGCGAGTTTGGGAGGCTCGCATTTGA 120
Db 394 GACCACCTTGAATTTTGGCGAGCCATTGGGAAAGGCGAGTTTGGGAGGCTCGCATTTGA 453
Qy 121 CAGAAGATGATACCAAGAGATGTACGCAATGAAGTACATGAATAAACAAAAGTGGGTG 180
Db 454 CAGAAGATGATACCAAGAGATGTACGCAATGAAGTACATGAATAAACAAAAGTGGGTG 513
Qy 181 GAGCGCAATGAAGTGAGAAATGCTTCAAGGAACTCAGATCATGAGGCTCTGGAGCAC 240
Db 514 GAGCGCAATGAAGTGAGAAATGCTTCAAGGAACTCAGATCATGAGGCTCTGGAGCAC 573
Qy 241 CCTTTCTCGTGAATTTTGTGTTTCTTCCAGATGAGGAAAGCATGTTTCATGGTGGTG 300
Db 574 CCTTTCTCGTGAATTTTGTGTTTCTTCCAGATGAGGAAAGCATGTTTCATGGTGGTG 633
Qy 301 GACCTCTCGTGGGTGAGACCTGCGTTATCACCTGCAACAGAAACGTCCTCAAGGAA 360
Db 634 GACCTCTCGTGGGTGAGACCTGCGTTATCACCTGCAACAGAAACGTCCTCAAGGAA 693

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Job time : 1592 secs

Qy 361 GAAACAGTGAAGCTCTTTTCATCTGTGAGCTGCTCATGGCCCTGGACTACCTGCAGAACCG 420
Db 694 GAAACAGTGAAGCTCTTTTCATCTGTGAGCTGCTCATGGCCCTGGACTACCTGCAGAACCG 753
Qy 421 CGCATCATTTACAGAGGATATGAAGCCTGACAAATATTTTACTTGAACGAAATGGGCACGTG 480
Db 754 CGCATCATTTACAGAGGATATGAAGCCTGACAAATATTTTACTTGAACGAAATGGGCACGTG 813
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Db 814 CACATCACAGATTTCAACATTTGCTGGATGCTGCCAGGAGAGACACAGATATACCACATG 873
Qy 541 GCTGGCAACCAAGCTTTACATTTGCTGGATGCTGCCAGGAGAGACACAGATATACCACATG 600
Db 874 GCTGGCAACCAAGCTTTACATTTGCTGGATGCTGCCAGGAGAGACACAGATATACCACATG 933
Qy 601 TCCTTTGCTGTTGACTGCTGGTCCCTGGGAGTGACGCGCATATGAACCTGCTGAGAGGCGG 660
Db 934 TCCTTTGCTGTTGACTGCTGGTCCCTGGGAGTGACGCGCATATGAACCTGCTGAGAGGCGG 993
Qy 661 AGACCGTATCATATTTGCTCCAGTACTTCCAGCAAGGAAATTTGTACACAGCTTTGAGACG 720
Db 994 AGACCGTATCATATTTGCTCCAGTACTTCCAGCAAGGAAATTTGTACACAGCTTTGAGACG 1053
Qy 721 ACTGTTGTAACCTTACCTCTGCTGTCACAGGAAATGCTGTCACCTTTCTTAAAAAGCTA 780
Db 1054 ACTGTTGTAACCTTACCTCTGCTGTCACAGGAAATGCTGTCACCTTTCTTAAAAAGCTA 1113
Qy 781 CTCGAAACCTAATCCAGACCAACGATTTTCTCAGTTATCTGATGTCCAGAACTTCCCGTAT 840
Db 1114 CTCGAAACCTAATCCAGACCAACGATTTTCTCAGTTATCTGATGTCCAGAACTTCCCGTAT 1173
Qy 841 ATGAATGATATAAAGCTGGGATGAGTTTTCAGAGAGGCTCATTCAGGTTTCATTCCT 900
Db 1174 ATGAATGATATAAAGCTGGGATGAGTTTTCAGAGAGGCTCATTCAGGTTTCATTCCT 1233
Qy 901 AATAAGGCGAGGCTGAATTTGATGCTTACCTTTGAACTTCAGGAAATGATTTTGGAGTCC 960
Db 1234 AATAAGGCGAGGCTGAATTTGATGCTTACCTTTGAACTTCAGGAAATGATTTTGGAGTCC 1293
Qy 961 AAAACCTCTACATAAGAAAAAAGCGCTCTGGCAAGAGAGAGGATATGAGGAAATGC 1020
Db 1294 AAAACCTCTACATAAGAAAAAAGCGCTCTGGCAAGAGAGAGGATATGAGGAAATGC 1353
Qy 1021 GATTCCTCTCAGACATG 1037
Db 1354 GATTCCTCTCAGGTAAG 1370

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 20, 2004, 04:50:53 ; Search time 91 Seconds
(without alignment)
9560.501 Million cell updates/sec

Title: US-10-620-845-8

Perfect score: 1224

Sequence: 1 atgggagccacacttcaag.....agacctggaagtctcataa 1224

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 35539441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:**
- 3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:**
- 4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:**
- 5: /cgn2_6/ptodata/1/ina/PTCUS.COMB.seq:**
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1165.4	95.2	1191	4	US-09-841-683-10
4	1160.6	94.8	1485	4	US-09-801-876B-1
5	1160.6	94.8	1485	4	US-10-254-869-1
6	661	54.0	711	4	US-09-841-683-6
7	660	53.9	678	4	US-09-841-683-4
8	484.8	39.6	1257	4	US-09-799-875-15
9	484.8	39.6	1257	4	US-09-799-875-13
10	470	38.4	1864	4	US-09-819-607-1
11	181.8	14.9	148567	4	US-09-801-876B-3
12	181.8	14.9	148567	4	US-10-254-869-3
13	134.2	11.0	1008	4	US-09-394-455-3
14	134.2	11.0	2549	3	US-09-467-082-3
15	134.2	11.0	2549	4	US-09-394-455-5
16	134.2	11.0	2608	4	US-09-394-455-35
17	134	10.9	819	4	US-09-270-767-1482
18	134	10.9	819	4	US-09-270-767-16764
19	133.6	10.9	1619	4	US-09-394-455-14
20	122.6	10.0	25603	4	US-09-819-607-3
21	121.4	9.9	1788	4	US-09-417-197-68
22	121.4	9.9	2211	4	US-09-394-455-39
23	120.4	9.8	1498	3	US-09-509-902A-6
24	120.4	9.8	1961	3	US-09-509-902A-15
25	120.4	9.8	2204	1	US-08-221-817-12
26	120.4	9.8	2204	1	US-08-454-439-12
27	120.4	9.8	2204	5	PCT-US94-10487-12

ALIGNMENTS

RESULT 1

US-09-841-683-8

; Sequence 8, Application US/09841683

; Patent No. 6617147

; GENERAL INFORMATION:

; APPLICANT: Hu, Yi

; APPLICANT: Nepomichy, Boris

; APPLICANT: Wang, Xiaoming

; APPLICANT: Donoho, Gregory

; APPLICANT: Scoville, John

; APPLICANT: Walke, D. Wade

; TITLE OF INVENTION: No. 6617147el Human Kinase Proteins and Polynucleotides Encoding

; FILE REFERENCE: LEX-0167-USA

; CURRENT APPLICATION NUMBER: US/09/841,683

; PRIOR FILING DATE: 2001-04-24

; PRIOR APPLICATION NUMBER: US 60/199,499

; PRIOR FILING DATE: 2000-04-25

; PRIOR APPLICATION NUMBER: US 60/201,227

; PRIOR FILING DATE: 2000-05-01

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 8

; LENGTH: 1224

; TYPE: DNA

; ORGANISM: homo sapiens

US-09-841-683-8

Query Match 100.0%; Score 1224; DB 4; Length 1224;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGGGAGCCACACTTCAAGAAACCCACAGTGTTCATGAAATGAAGATGTCACACTTT	60
Db	1	ATGGGAGCCACACTTCAAGAAACCCACAGTGTTCATGAAATGAAGATGTCACACTTT	60
Qy	61	GACCACCTTGAAATTTTGGGAGCCATTTGGGAAAGCCAGTTTGGGAAAGTCTGCATTGTA	120
Db	61	GACCACCTTGAAATTTTGGGAGCCATTTGGGAAAGCCAGTTTGGGAAAGTCTGCATTGTA	120
Qy	121	CAGAAGATGATCAACAAAGAGATGTACGCAATGAAGTACATGAATAAACAAGTGCCTG	180
Db	121	CAGAAGATGATCAACAAAGAGATGTACGCAATGAAGTACATGAATAAACAAGTGCCTG	180
Qy	181	GAGGCGAATGAGTGAAGATGTTCTTCAAGAACTCCAGATCATGCAGGCTCTGGAGCAC	240
Db	181	GAGGCGAATGAGTGAAGATGTTCTTCAAGAACTCCAGATCATGCAGGCTCTGGAGCAC	240
Qy	241	CTTTTCTGGTTAATTTTGTGTATTCCTTCCAAGATGAGGAAGACATGTTTCATGTTGTTG	300
Db	241	CTTTTCTGGTTAATTTTGTGTATTCCTTCCAAGATGAGGAAGACATGTTTCATGTTGTTG	300

QY	301	GACCTCTGCTGGTGGAGACCTCGTTATCACTGCAACAGAACGTCCTCACTTCAAGGAA	360
DB	301		
QY	361	GAACAGTGAAGCTCTTCACTGTGAGCTGTATGCGCTTATCACTGCAACAGAACGTCCTCAAGGAA	420
DB	361		
QY	421	CGCATCTTCAACAGGATATGAAGCTTGACAAATATTTTACTGTACGAACATGGGACGCTG	480
DB	421		
QY	481	CACATCACAGATTTCAACATTTCTGCGATGCTGCCAGGAGACACAGATTTACCACCATG	540
DB	481		
QY	541	GCTGGCACCAAGCCTTACATGGCACTTGAGATGTTTCACTCCAGAAAGGACGAGGCTAT	600
DB	541		
QY	601	TCCCTTTGCTGTGACTGTGGTGCCTGGAGTGACGGCATATGAATCTCTGAGAGGCGGG	660
DB	601		
QY	661	AGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTTGATCAACAGCTTTGAGACG	720
DB	661		
QY	721	ACTGTTGTAACCTTACCTTCTGCTGGTCAACAGGAAATGGTGCTCACTTTTAAAGGCTA	780
DB	721		
QY	781	CTCGAACCTTAATCCAGACCAAGATTTCTGAGTATCTGATGTCAGAACTTCCCGTAT	840
DB	781		
QY	841	ATGAAATGATATAAATCGGATGAGTCTTTCAGAGAGGCTCATTTCCAGGTTTCAATTCCT	900
DB	841		
QY	901	AATAAAGGAGGCTGAATTTGTGATCTCACTTTGAATCTTGAGAAATGATTTGGAGTCC	960
DB	901		
QY	961	AAACCTCTACATAAGAAAGGCTCTGGCAAGAGAGGATATGAGGAAATGC	1020
DB	961		
QY	1021	GATTTCTCTCAGACATGCTCTTCTTCAAGAGCACCTTGACTCTGTCCAGAGGAGTTTCA	1080
DB	1021		
QY	1081	ATTTTCAACAGAGAAAGTAAACAGGACTTTTAAACAGAGACCAATCTTCGCTTG	1140
DB	1081		
QY	1141	GAACAAACCAAGACCCACAGTGAATAATGGACAAATGGACAAATGGACACAGGACTCT	1200
DB	1141		
QY	1201	TTTCAGACCTCGAAAGTTTCAATA	1224
DB	1201		
QY	1201	TTTCAGACCTCGAAAGTTTCAATA	1224
DB	1201		
RESULT 2			
US-09-841-683-12			
; Sequence 12, Application US/09841683			
; Patent No. 6617147			
; GENERAL INFORMATION:			
; APPLICANT: Hu, Yi			
; APPLICANT: Nepomnichy, Boris			

APPLICANT:	Wang, Xiaoming
APPLICANT:	Donoho, Gregory
APPLICANT:	Scoville, John
APPLICANT:	Walke, D. Wade
TITLE OF INVENTION:	No. 6617147el Human Kinase Proteins and Polynucleotides Encoding
FILE REFERENCE:	LEX-0167-USA
CURRENT APPLICATION NUMBER:	US/09/841,683
CURRENT FILING DATE:	2001-04-24
PRIOR APPLICATION NUMBER:	US 60/199,499
PRIOR FILING DATE:	2000-04-25
PRIOR APPLICATION NUMBER:	US 60/201,227
PRIOR FILING DATE:	2000-05-01
NUMBER OF SEQ ID NOS:	12
SOFTWARE:	FastSeq for Windows Version 4.0
SEQ ID NO 12	
LENGTH:	1675
TYPE:	DNA
ORGANISM:	homo sapiens
	US-09-841-683-12

Query Match	100.0%;	Score 1224;	DB 4;	Length 1675;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1224;	Conservative	0;	Mismatches	0;
Indels	0;	Gaps	0;	

QY	1	ATGGGAGCCAACTTCAAGAAACCCACGAGTGTGATGAAATGAAGATGTCAACTTT	60
DB	413	ATGGGAGCCAACTTCAAGAAACCCACGAGTGTGATGAAATGAAGATGTCAACTTT	472
QY	61	GACCACTTTGAAATTTTGGAGCCATTGGGAAAGGAGTGTGGGAAAGTCTGCAATTGTA	120
DB	473	GACCACTTTGAAATTTTGGAGCCATTGGGAAAGGAGTGTGGGAAAGTCTGCAATTGTA	532
QY	121	CAGAAGAAATGATACCAAGAAAGATGTAGCAATGAAGTACATGAATATAAAGTGGTG	180
DB	533	CAGAAGAAATGATACCAAGAAAGATGTAGCAATGAAGTACATGAATATAAAGTGGTG	592
QY	181	GAGCGCAATCAAGTGAAGATGTCTCAAGAACTCCAGATCATGATGAGGCTCTGGAGCAC	240
DB	593	GAGCGCAATCAAGTGAAGATGTCTCAAGAACTCCAGATCATGATGAGGCTCTGGAGCAC	652
QY	241	CTTTCTCTGTTAATTTTGTGTTATCTTCAAGATGAGGAAACATGTTTCAATGTTGGTG	300
DB	653	CTTTCTCTGTTAATTTTGTGTTATCTTCAAGATGAGGAAACATGTTTCAATGTTGGTG	712
QY	301	GACCTCTGCTGGTGGAGACCTTCACTGAGCTGCTGATGAGGCTGAGGCTGAGGCTG	360
DB	713	GACCTCTGCTGGTGGAGACCTTCACTGAGCTGCTGATGAGGCTGAGGCTGAGGCTG	772
QY	361	GAACAGTGAAGCTCTTCACTGAGCTGCTGATGAGGCTGAGGCTGAGGCTGAGGCTG	420
DB	773	GAACAGTGAAGCTCTTCACTGAGCTGCTGATGAGGCTGAGGCTGAGGCTGAGGCTG	832
QY	421	CGCATATTCACAGGATATGAGCCTGAGCAATATTTTCTGACGAAACATGGGACGCTG	480
DB	833	CGCATATTCACAGGATATGAGCCTGAGCAATATTTTCTGACGAAACATGGGACGCTG	892
QY	481	CACATCACAGATTTCAACATTTCTGCGATGCTGCCAGGAGACACAGATTTACCACATG	540
DB	893	CACATCACAGATTTCAACATTTCTGCGATGCTGCCAGGAGACACAGATTTACCACATG	952
QY	541	GCTGGCACCAAGCCTTACATGGCACTTGAGATGTTTCACTCCAGAAAGGACGAGGCTAT	600
DB	953	GCTGGCACCAAGCCTTACATGGCACTTGAGATGTTTCACTCCAGAAAGGACGAGGCTAT	1012
QY	601	TCCTTTGCTGTGATGTTGTTGCTTCCCTGGAGTACGCGCATATGAATCTCTGAGAGGCGG	660
DB	1013	TCCTTTGCTGTGATGTTGTTGCTTCCCTGGAGTACGCGCATATGAATCTCTGAGAGGCGG	1072
QY	661	AGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTTGATCAACAGCTTTGAGACG	720
DB	1073	AGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTTGATCAACAGCTTTGAGACG	1132
QY	721	ACTGTTGTAACCTTACCTTCTGCTGGTCAACAGGAAATGGTGCTCACTTTTAAAGGCTA	780


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Db 1133 ACTGTTGTAACCTTCTGCTGTCACAGGAAATGGTGTCACTTCTTAAAGCTA 1192
Qy 781 CTCGAACCTAATCAGAACCAACGATTTCTCAGTTATCTGATGTCCAGAACTTCCCGTAT 840
Db 1193 CTCGAACCTAATCAGAACCAACGATTTCTCAGTTATCTGATGTCCAGAACTTCCCGTAT 1252
Qy 841 ATGAATCATATAAATCGGATGCAAGTTTTCAGAAAGAGGCTCATTCAGGTTTCATTCCT 900
Db 1253 ATGAATCATATAAATCGGATGCAAGTTTTCAGAAAGAGGCTCATTCAGGTTTCATTCCT 1312
Qy 901 AATAAAGCGAGCTGAATTTGATGCTTACCTTTTGAACCTTGAGGAAATGATTTTGGAGTCC 960
Db 1313 AATAAAGCGAGCTGAATTTGATGCTTACCTTTTGAACCTTGAGGAAATGATTTTGGAGTCC 1372
Qy 961 AAACCTCTACATAAGAAAAAAGCGTCTGCGCAAGAGAGGAAAGGATATGAGGAAATGC 1020
Db 1373 AAACCTCTACATAAGAAAAAAGCGTCTGCGCAAGAGAGGAAAGGATATGAGGAAATGC 1432
Qy 1021 GATTCCTCTCAGACATGCTTCTTCAAGAGCAGCTTGAACCTTGCTCTGTCAGAGGATTCATA 1080
Db 1433 GATTCCTCTCAGACATGCTTCTTCAAGAGCAGCTTGAACCTTGCTCTGTCAGAGGATTCATA 1492
Qy 1081 ATTTTCAACAGAAAAAGTAAACAGGAGCTTTTAAACAAAGACAAACAAATCTAGCCTTG 1140
Db 1493 ATTTTCAACAGAAAAAGTAAACAGGAGCTTTTAAACAAAGACAAACAAATCTAGCCTTG 1552
Qy 1141 GAACAAACCAAGACCCACCAAGTGAACAAATGGACAAATGGACAAATGGACAAATGGACAA 1200
Db 1553 GAACAAACCAAGACCCACCAAGTGAACAAATGGACAAATGGACAAATGGACAAATGGACAA 1612
Qy 1201 TTTGAGACCTCGAAAGTTTCATAA 1224
Db 1613 TTTGAGACCTCGAAAGTTTCATAA 1636

RESULT 3
US-09-841-683-10
; Sequence 10, Application US/09841683
; Patent No. 6617147
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Nepomichy, Boris
; APPLICANT: Wang, Xiaoming
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Walke, D. Wade
; TITLE OF INVENTION: No. 6617147el Human Kinase Proteins and Polynucleotides Encoding
; FILE REFERENCE: LEX-0167-USA
; CURRENT APPLICATION NUMBER: US/09/841,683
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: US 60/199,499
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US 60/201,227
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 1191
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-841-683-10

Query Match 95.2%; Score 1165.4; DB 4; Length 1191;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 1172; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 1 ATGGAGGACCAACTTCAAGAAAAACCAACGAGTGTGATGAAAAATGAAGATGTCAACTTT 60
Db 1 ATGGAGGACCAACTTCAAGAAAAACCAACGAGTGTGATGAAAAATGAAGATGTCAACTTT 60
Qy 61 GACCACTTTGAAATTTTCGAGGCCATTTGGGAAAGGCACTTTTGGGAAGGCTCTGCAATTGTA 120
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61 GACCACTTTGAAATTTTTCGAGGCCATTTGGGAAAGGCACTTTTGGGAAGGCTCTGCAATTGTA 120
121 CAGAAGAAATGATACCAAGAAGATGTACGCAATGAAGTACATGAATAAACAAGAGTGGTG 180
121 CAGAAGAAATGATACCAAGAAGATGTACGCAATGAAGTACATGAATAAACAAGAGTGGTG 180
181 GAGCGCAATGAAGTGAAGAAATGCTTCAAGAACTCCAGATCATGAGGGTCTCGAGCAC 240
181 GAGCGCAATGAAGTGAAGAAATGCTTCAAGAACTCCAGATCATGAGGGTCTCGAGCAC 240
241 CTTTCTCTGTTAAATTTGTTGGTATTCCTTCAAGATGAGGAAGACATGTTTCATGGTGGT 300
241 CTTTCTCTGTTAAATTTGTTGGTATTCCTTCAAGATGAGGAAGACATGTTTCATGGTGGT 300
301 GACCTCTCTGTTGGTGAAGACCTGCGTTATCACCTGCAACAGACCTCCACTTCAAGGAA 360
301 GACCTCTCTGTTGGTGAAGACCTGCGTTATCACCTGCAACAGACCTCCACTTCAAGGAA 360
361 GAAACAGTGAAGCTCTTTCATCTGTGAGCTGCTGATGCCCTGGACTACCTGCAAAACAG 420
361 GAAACAGTGAAGCTCTTTCATCTGTGAGCTGCTGATGCCCTGGACTACCTGCAAAACAG 420
421 CGCATCAATTCACAGGGATATGAAGCCTGACAAATATTTTACTTGAACCAATGGGCACTG 480
421 CGCATCAATTCACAGGGATATGAAGCCTGACAAATATTTTACTTGAACCAATGGGCACTG 480
481 CACATCAAGATTTCAACATTTGCTGCGATGCTGCCAGGGAGACACAGATTTACCAACATG 540
481 CACATCAAGATTTCAACATTTGCTGCGATGCTGCCAGGGAGACACAGATTTACCAACATG 540
541 GCTGGCACCAAGCTTACATGCGACCTGAGATGTTTCTGATGCCCAAGAAAGGAGGCTAT 600
541 GCTGGCACCAAGCTTACATGCGACCTGAGATGTTTCTGATGCCCAAGAAAGGAGGCTAT 600
601 TCCTTTGCTGTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
601 TCCTTTGCTGTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
661 AGACCGTATCATATTCCTCCAGTACTTCCAGCAAGGAAATTTGACACACCTTTGAGACG 720
661 AGACCGTATCATATTCCTCCAGTACTTCCAGCAAGGAAATTTGACACACCTTTGAGACG 720
721 ACTGTTGTAACCTTACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
721 ACTGTTGTAACCTTACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
781 CTCGAACCTAATCCAGAACCAACGATTTTCTCAGTTATCTGATGTCCAGAACTTCCCGTAT 840
781 CTCGAACCTAATCCAGAACCAACGATTTTCTCAGTTATCTGATGTCCAGAACTTCCCGTAT 840
841 ATGAATCATATAAATCGGATGCAAGTTTTCAGAAAGAGGCTCATTCAGGTTTCATTCCT 900
841 ATGAATCATATAAATCGGATGCAAGTTTTCAGAAAGAGGCTCATTCAGGTTTCATTCCT 900
901 AATAAAGCGAGCTGAATTTGATGCTTACCTTTTGAACCTTGAGGAAATGATTTTGGAGTCC 960
901 AATAAAGCGAGCTGAATTTGATGCTTACCTTTTGAACCTTGAGGAAATGATTTTGGAGTCC 960
961 AAACCTCTACATAAGAAAAAAGCGTCTGCGCAAGAGAGGAAAGGATATGAGGAAATGC 1020
961 AAACCTCTACATAAGAAAAAAGCGTCTGCGCAAGAGAGGAAAGGATATGAGGAAATGC 1020
1021 GATTCCTCTCAGACATGCTTCTTCAAGAGCAGCTTGAACCTTGCTCTGTCAGAGGATTCATA 1080
1021 GATTCCTCTCAGACATGCTTCTTCAAGAGCAGCTTGAACCTTGCTCTGTCAGAGGATTCATA 1080
1081 ATTTTCAACAGAAAAAGTAAACAGGAGCTTTTAAACAAAGACAAACCAATCTAGCCTTG 1140
1081 ATTTTCAACAGAAAAAGTAAACAGGAGCTTTTAAACAAAGACAAACCAATCTAGCCTTG 1140
1141 GAACAAACCAAGACCCACCAAGTGAACAAATGGACAAATGGACAAATGGACAAATGGACAA 1183
1141 GAACAAACCAAGACCCACCAAGTGAACAAATGGACAAATGGACAAATGGACAAATGGACAA 1183
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RESULT 4
US-09-801-876B-1
; Sequence 1, Application US/09801876B
; Patent No. 6492155
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001160
; CURRENT APPLICATION NUMBER: US/09/801,876B
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1485
; TYPE: DNA
; ORGANISM: Human
US-09-801-876B-1

Query Match      94.8%; Score 1160.6; DB 4; Length 1485;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 1169; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY      1  ATGGAGGCAACACACTTCAAGAAACCAACAGTGTGATGAAATGAAGATGTCAACTTT 60
DB      1  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      3  ATGGAGGCAACACTTCAAGAAACCAACAGTGTGATGAAATGAAGATGTCAACTTT 62
DB      3  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      61  GACCACTTTGAAATTTTGGAGGCAATTCGGAAGGCACTTTTGGAGGCTGCAATGTA 120
DB      61  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      63  GACCACTTTGAAATTTTGGAGGCAATTCGGAAGGCACTTTTGGAGGCTGCAATGTA 122
DB      63  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      121  CAGAGATGATACCAAGAGATGTACCAATGAATGATGATGATGATGATGATGATGATG 180
DB      121  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      123  CAGAGATGATACCAAGAGATGTACCAATGAATGATGATGATGATGATGATGATGATG 182
DB      123  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      181  GAGCGCAATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240
DB      181  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      183  GAGCGCAATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 242
DB      183  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Query Match      94.8%; Score 1160.6; DB 4; Length 1485;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 1169; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY      1  ATGGAGGCAACACACTTCAAGAAACCAACAGTGTGATGAAATGAAGATGTCAACTTT 60
DB      1  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      3  ATGGAGGCAACACTTCAAGAAACCAACAGTGTGATGAAATGAAGATGTCAACTTT 62
DB      3  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      61  GACCACTTTGAAATTTTGGAGGCAATTCGGAAGGCACTTTTGGAGGCTGCAATGTA 120
DB      61  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      63  GACCACTTTGAAATTTTGGAGGCAATTCGGAAGGCACTTTTGGAGGCTGCAATGTA 122
DB      63  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      121  CAGAGATGATACCAAGAGATGTACCAATGAATGATGATGATGATGATGATGATGATG 180
DB      121  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      123  CAGAGATGATACCAAGAGATGTACCAATGAATGATGATGATGATGATGATGATGATG 182
DB      123  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      181  GAGCGCAATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240
DB      181  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      183  GAGCGCAATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 242
DB      183  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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QY      721  ACTGTGTAACTTACCTTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 780
DB      721  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      781  CTCGAACCTAATCCAGACCAACGATTTTCTCAGTTATCTGTATGTCCAGAACTTCCCGTAT 840
DB      781  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      841  ATGAATGATATAAACTGGGATGAGTTTTCAGAAAGAGGCTCATTCAGAGTTTCATTCCT 900
DB      841  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      901  AATAAGGCGAGGCTGAATTTGTATCTTACCTTTTGAACCTTGTGAAGAAATGATTTTGAGTCC 960
DB      901  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      961  AAACCTCTACATATAAGAAAGGCTTGTGCAAGAGGAGGAGGATATGAGAAATGC 1020
DB      961  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      1021  GATTTCTTCTCAGACATGTCTTCTCAAGAGCACCTTGTCTGTCCAGAGGAGTTCATA 1080
DB      1021  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      1081  ATTTTCAACAGAGAAAAAGTAAACAGGACCTTTTAAACAAAGAACCAACCAATCTAGCCTTG 1140
DB      1081  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      1141  GAACAAACCAAGAGACCCACAGTCAACAAATGGACAAATGACA 1183
DB      1141  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      1143  GAACAAACCAAGAGACCCACAGTCAACAAATGGATGGTTCAGAAATACA 1185
DB      1143  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 5
US-10-254-869-1
; Sequence 1, Application US/10254869
; Patent No. 6653117
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001160DIV
; CURRENT APPLICATION NUMBER: US/10/254,869
; CURRENT FILING DATE: 2002-09-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1485
; TYPE: DNA
; ORGANISM: Human
US-10-254-869-1

Query Match      94.8%; Score 1160.6; DB 4; Length 1485;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 1169; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY      1  ATGGAGGCAACACTTCAAGAAACCAACAGTGTGATGAAATGAAGATGTCAACTTT 60
DB      1  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      3  ATGGAGGCAACACTTCAAGAAACCAACAGTGTGATGAAATGAAGATGTCAACTTT 62
DB      3  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      61  GACCACTTTGAAATTTTGGAGGCAATTCGGAAGGCACTTTTGGAGGCTGCAATGTA 120
DB      61  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      63  GACCACTTTGAAATTTTGGAGGCAATTCGGAAGGCACTTTTGGAGGCTGCAATGTA 122
DB      63  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      121  CAGAGATGATACCAAGAGATGTACCAATGAATGATGATGATGATGATGATGATGATG 180
DB      121  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      123  CAGAGATGATACCAAGAGATGTACCAATGAATGATGATGATGATGATGATGATGATG 182
DB      123  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      181  GAGCGCAATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240
DB      181  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      183  GAGCGCAATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 242
DB      183  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```



```
RESULT 7
US-09-841-683-4
; Sequence 4, Application US/09841683
; Patent No. 6617147
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Nepomnichy, Boris
; APPLICANT: Wang, Xiaoming
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Walke, D. Wade
; TITLE OF INVENTION: No. 6617147el Human Kinase Proteins and Polynucleotides Encoding
; FILE REFERENCE: LEX-0167-USA
; CURRENT APPLICATION NUMBER: US/09/841,683
; CURRENT FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: US 60/159,499
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US 60/201,227
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 678
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-841-683-4

Query Match      53.9%; Score 660; DB 4; Length 678;
Best Local Similarity 100.0%; Pred. No. 4e-206;
Matches 660; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGAGCCACCTTCAGAAAGAACCCACGAGTGTGTGATGAAATGAAGATGTCAACTTT 60
DB 1 ATGGGAGCCACCTTCAGAAAGAACCCACGAGTGTGTGATGAAATGAAGATGTCAACTTT 60
QY 61 GACCACTTTGAAATTTTGGAGCCATTGGGAAGCCAGTTTGGGAAGTCTGCATTGTA 120
DB 61 GACCACTTTGAAATTTTGGAGCCATTGGGAAGCCAGTTTGGGAAGTCTGCATTGTA 120
QY 121 CAGAGAATGATACCAAGAGATGTACGCAATGAAGTGAATGATCAATATAAACAAGTGCCTG 180
DB 121 CAGAGAATGATACCAAGAGATGTACGCAATGAAGTGAATGATCAATATAAACAAGTGCCTG 180
QY 181 GAGCGAATGAGTGAAGTGAAGTCTTCAAGAACTCCAGATCATGCGAGGCTCGAGCAC 240
DB 181 GAGCGAATGAGTGAAGTGAAGTCTTCAAGAACTCCAGATCATGCGAGGCTCGAGCAC 240
QY 241 CCTTTCCTGGTTAAATTTGTGGTATTCCTTCCAGATGAGGAAGACATGTTTCAATGGTGTG 300
DB 241 CCTTTCCTGGTTAAATTTGTGGTATTCCTTCCAGATGAGGAAGACATGTTTCAATGGTGTG 300
QY 301 GACCTCTCTGGTGGAGACCTGGTATATCACTTCAAGAAAGAGCTTCAACTTCAAGGAA 360
DB 301 GACCTCTCTGGTGGAGACCTGGTATATCACTTCAAGAAAGAGCTTCAACTTCAAGGAA 360
QY 361 GAAACAGTGAAGCTTTCATCTGTCAGCTGTGTCAGCCCTGAGTACCTTCAGAACAG 420
DB 361 GAAACAGTGAAGCTTTCATCTGTCAGCTGTGTCAGCCCTGAGTACCTTCAGAACAG 420
QY 421 CCATCATTCAGGGATATGAAGCTTGACATATTTTACTTTGACGAACATGGGCACGTG 480
DB 421 CCATCATTCAGGGATATGAAGCTTGACATATTTTACTTTGACGAACATGGGCACGTG 480
QY 481 CACATCAGATTTCAATGCTGCGATGTCGCCAGGGAGACACAGATTTACCAACATG 540
DB 481 CACATCAGATTTCAATGCTGCGATGTCGCCAGGGAGACACAGATTTACCAACATG 540
QY 541 GCTGSCACCAAGCCTTACATGCGACCTGAGATGTTTCACTTCCAGAAAGGAGGAGGCTAT 600
DB 541 GCTGSCACCAAGCCTTACATGCGACCTGAGATGTTTCACTTCCAGAAAGGAGGAGGCTAT 600
QY 601 TCCTTTGCTGTGATGTGTGCTTGGAGTGAAGCGCATATGAATCTCTGAGAGGCCGG 660
DB 601 TCCTTTGCTGTGATGTGTGCTTGGAGTGAAGCGCATATGAATCTCTGAGAGGCCGG 660
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Db 601 TCCTTTGCTGTGATGTGTGCTTGGAGTGAAGCGCATATGAATCTCTGAGAGGCCGG 660

RESULT 8
US-09-799-875-15
; Sequence 15, Application US/09799875
; Patent No. 6638721
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Williamson, Mark
; TITLE OF INVENTION: No. 6638721el Human Protein Kinases and Uses
; FILE REFERENCE: 35800/209996
; CURRENT APPLICATION NUMBER: US/09/799,875
; CURRENT FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 60/182,059
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 09/659,287
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-799-875-15
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Query Match      39.6%; Score 484.8; DB 4; Length 1257;
Best Local Similarity 66.7%; Pred. No. 2.2e-148;
Matches 728; Conservative 0; Mismatches 352; Indels 12; Gaps 2;

QY 28 CCAGTGTTCATGAATGAAGATGATCACTTTGACCACTTTGAAATTTTGGAGCCATT 87
DB 37 CCGTGTGTTGACCAAGGAGGACGTAATTCGACACTTCAGATCTCTCGGGCATT 96
QY 88 GGGAAAGGCGAGTTTGGGAAGTCTGCAATGTGACAGAAGATCATACCAAGAAGATGTAC 147
DB 97 GGGAAAGGCGAGTTTGGCAAGTGTGCAATGTGACAGAAGGCGGACAGGAGATGTAC 156
QY 148 GCATGAAGTACATGAATATAAAGTGTGCGTGGAGGCAATGAAGTGAAGATGTCTTC 207
DB 157 GCCATGAAGTACATGAATATAAAGTGTGCGTGGAGGCAATGAAGTGAAGATGTCTTC 216
QY 208 AAGGAATCCAGATCATGAGGCTCTGGAGCACCTTCTGCTGTTAATTTGGTATTCC 267
DB 217 CGGAGCTGAGATCTTCAAGGAGTCAAGCACTTCTGCTGTTAATTTGGTATTCC 276
QY 268 TTCCAAGTGAAGAGACATGTTTCAATGTGTGGACCTCTCTGCTGTTGAGACCTTCGCT 327
DB 277 TTCAGAGCAGGAGGACATGTTTCAATGTGTGGACCTCTCTGCTGTTGAGACCTTCGCT 336
QY 328 TATCAGCTGCAAGAGCCTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 387
DB 337 TACCACTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 396
QY 388 CTGGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 447
DB 397 ATGGCACTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 456
QY 448 GACATATTTTACTTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 507
DB 457 GACATATTTTACTTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 516
QY 508 ATGCTGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 567
DB 517 ATCATCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 576
QY 568 GAGATGTTTCAAGTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 621
DB 577 GAGATGTTTCAAGTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 636
QY 622 TCCTTGGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 681
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Db 637 TCGTGGGGTGATGGCTATAGCTGCTCGAGATGGAGGCCCTATGACATCCACTCC 696
Qy 682 AGTACTTCCAGCAAGGAAATGTAACACAGCTTTGAGACGACTGTGTGAATTAACCTTCT 741
Db 697 AGCAACGCGGTGGAGTCCCTGGTGCAGCTGTTCAGCAACCGTGAGCGTCCAGTATGTCCCC 756
Qy 742 GCCTGTGCACAGGAATGGTGTCACTTCTTAAAGCTACTCGAACCTTAATCCAGACCA 801
Db 757 ACGTGGTCCAGGAGATGGTGGCCCTTGTGCGAAGCTTCTCACTGTGAACCCCGAGCAC 816
Qy 802 CGATTTTCTCAGTTATCTGTATGTCCAGAACTTCCCGTATATGAATGATATAAACTGGGAT 861
Db 817 CGGTCTCCAGCTCCAGGAGTGCAGCGACCCCGCGGCTGGCGGCTGCTGTGGAC 876
Qy 862 GCAGTTTTCAGAGAGGCTCAITTCAGGTTTCAATTCCTAATAAAGGAGGCTGAATGT 921
Db 877 CACCTGAGCGAGAGAGGCTGGAGCGCGGCTTCGTGCGAAGCTTCTCACTGTCACTGC 936
Qy 922 GATCCTACCTTTGAATCTGAGGAATGATTTTGAGTCCAAACCTCTACATAAGAAAA 981
Db 937 GACCCACCTTTGAGCTGGAGGAGATGATCTGAGTCCAGGCCCTGCACAAAGAAG 996
Qy 982 AAGCGTCTGCAAGAGAGGA-----GAAGGATATAGGAATGCGATTCTCTCAGACA 1035
Db 997 AAGGTCTGCGCAGAACAGTCCCGGGAACAGCAGGAGGACGCTCCAGTCCGAGAT 1056
Qy 1036 TGTCTTCTCAAGAGCACCTTGACTCTGTGTCAGAGGAGTTCAATAATTTTCAACAGAGAA 1095
Db 1057 GACTATCTTCAAGACTGCTCGATGCCATCCAGCAAGACTTCGTGATTTTTTAAACAGAGAA 1116
Qy 1096 AAGTAAACAGG 1107
Db 1117 AAGCTGAAGAGG 1128
```

RESULT 9

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US-09-799-875-13
; Sequence 13, Application US/09799875
; Patent No. 6638721
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Williamson, Mark
; TITLE OF INVENTION: No. 6638721el Human Protein Kinases and Uses
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: 35800/209996
; CURRENT APPLICATION NUMBER: US/09/799,875
; CURRENT FILING DATE: 2001-03-06
; PRIOR FILING DATE: 60/182,059
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 09/659,287
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 1826
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (17)...(1273)
US-09-799-875-13
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Query Match 39.6%; Score 484.8; DB 4; Length 1826;
Best Local Similarity 66.7%; Pred. No. 3e-148;
Matches 728; Conservative 0; Mismatches 352; Indels 12; Gaps 2;

Qy 28 CCACTGTTTGATGAAATGAAGATGTCACCTTTGACCACTTTGAAATTTTCGAGCCATT 87
Db 53 CCGGTGTTTGACACAGGAGGAGCGTGAATTCGACCACTTCCAGATCTTCGGGCCATT 112
Qy 88 GGGAAAGGCAGTTTTGGAGGCTGTCATTTGTACAGAAAGATGATACCAAGAAAGTGTAC 147
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RESULT 10

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Db 113 GGGAAAGGCAGTTTTGGCAAGGTGTGCAATTTGTGCAAGCGGAGACACGGAGAAGATGTAC 172
Qy 148 GCAATGAAGTACATGAATAAAACAAAAGTGGTGGAGCGCAATGAAGTGAGAAAATGTCTTTC 207
Db 173 GCCATGAAGTACATGAATAAAACAAAAGTGGTGGAGCGCAATGAAGTGAGAAAATGTCTTTC 232
Qy 208 AAGGAATCTCCAGATCATGCAAGGTGCTGAGGACCCCTTTCTTGGTTAAATTTGTGGTATTCC 267
Db 233 CGGAGCTGGAGATCTTCCAGGAGATCGAGCACCTTCTTGGTGAACCTCTGGTACTTCC 292
Qy 268 TTCCAGATGAGGAAGACATGTTTCATGCTGTGAGCACTCTCTGCTGGGTGGAGACCTGCGT 327
Db 293 TTCCAGGACGAGGAGACATGTTTCATGCTGTGAGCACTCTTACTTGGGGGGGACCTGCGC 352
Qy 328 TATCACCCTGCAACAGAAAGCTCCACTTCAAGGAAGAAACAGTGAAGCTCTTTCATCTGTGAG 387
Db 353 TACCACCCTGCAAGAAAGCTGCAAGTTCTCCAGGAGACACGGGTGAGGCTGTACATCTGCGAG 412
Qy 388 CTGCTCATGCGCCCTGGACTACCTGCAGAAACAGCGGCATCTTACACAGGGATATCAAGCCT 447
Db 413 ATGGCACTGGCTCTGGACTACCTGCGCGGCAGCACATATCCACAGAGATGTCAAGCCT 472
Qy 448 GACAATATTTTACTTGAAGAACATGGGCAGCTGCACATCAAGATTTTCAACATTTCTGTCG 507
Db 473 GACAACTTCTCTGGATGAGAGGAGATGCACACCTGACCGACTTCAACATTTGCCACC 532
Qy 508 ATGCTGCCAGGAGACACAGATTAACCATGCTGGCAACCAAGCTTACATGGCACCT 567
Db 533 ATCATCAAGACGCGGAGCGGCGACGCAATTAGCAGGCACCAAGCGCTACATGGCTCCG 592
Qy 568 GAGATGTTTCACTC-----CAGAAAGGAGCAGGCTATTTCTTGTGTTGACTGGTG 621
Db 593 GAGATCTTCCACTTTTGTCAACGCGCGGACCGGCTACTCTCTTCGAGGTGGACTGGTG 652
Qy 622 TCCCTGGGAGTGACGGCATATGAACCTGAGAGCGCGGAGACCGCTATCATATTTCGCTCC 681
Db 653 TCGTGGGGGTGATGGCTATGAGCTGCTGCGAGATGGAGGCCCTATGACATCCACTCC 712
Qy 682 AGTACTTCCAGCAAGGAAATTTGTACACAGCTTTGAGACGACTGTGTGTAACCTTACCCCTTCT 741
Db 713 AGCAACGCGCTGGAGTCCCTGGTGCAGCTGTTTCAGCACCCGTCGAGCGTCCAGTATGTCCCC 772
Qy 742 GCCTGGTCAAGGAAATGGTGTCACTTTTAAAGCTACTCGAACCTTAATCCAGACCA 801
Db 773 ACCTGGTCCAAGGAGATGCTGGCCCTTCTGCGGAAAGCTCTCTCACTGTCAACCCCGAGCAC 832
Qy 802 CGATTTTCTCAGTTTATCTGATGTCAGAACTTCCAGAACTTCCCGTATATGAATGATATAAACTGGGAT 861
Db 833 CGGCTCTCCAGCTCCAGGACGTGCGAGCGCCCGGGCTGGCGGGGCTGCTGTGGAC 892
Qy 862 GCAGTTTTTTCAGAGAGGCTCATTTCCAGGTTTTCATTTCTTAATAAAGGAGGCTGAATGT 921
Db 893 CACCTGAGCGAGAAAGAGGCTGGAGCGCGGCTTCTGCGCCCAACAAAGGCGCTGCACTGC 952
Qy 922 GATCTACCTTTGAACTTGAGGAAATGATTTTGAGTCCAAACCTCTACATAAGAAAA 981
Db 953 GACCCCACTTTGAGCTGGAGGAGATGATCTCTGAGTCCAGGCCCTGCACAAAGAAG 1012
Qy 982 AAGCGTCTGCAAGAAAGGA-----GAAGGATATAGGAATGCGATTCTTCTCAGACA 1035
Db 1013 AAGCTCTGCGCAAGAAACAGTCCCGGGAACACAGCAGGAGACAGTCCAGTCCGAGAT 1072
Qy 1036 TGTCTTCTCAAGAGCACCTTGTGCTGTCAGAGGAGTTTCAATAATTTTCAACAGAGAA 1095
Db 1073 GACTATCTTCAAGACTGCTCGATGCCATCCAGCAAGACTTTCGTGATTTTTTAAACAGAGAA 1132
Qy 1096 AAGTAAACAGG 1107
Db 1133 AAGCTGAAGAGG 1144
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US-09-819-607-1
; Sequence 1, Application US/09819607
; Patent No. 6686176
; GENERAL INFORMATION:
; APPLICANT: BEASLEY, Ellen et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001078
; CURRENT APPLICATION NUMBER: US/09/819,607
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1864
; TYPE: DNA
; ORGANISM: Human
; US-09-819-607-1

```

Query Match	38.4%	Score 470;	DB 4;	Length 1864;
Best Local Similarity	66.1%	Pred. No. 2.2e-143;		
Matches 715;	Conservative	0;	Mismatches 355;	Indels 12;
				Gaps 2;

QY	38	ATGAAATAGAGATGTCACCTTTGACCACTTTGAAATTTTCGAGACCAATGGGAAGGCA	97
Db	89	AAGCAGAGAAGGCAGTAGTGAATCTTCACCACTTCCAGATCTTCGGGCCATTTGGGAAGGCA	148
QY	98	GTTTTGGGAAGGTCTGCATTCTCAGAGAATGATACCAAGAAGATGTACGCATGAAGT	157
Db	149	GCITTTGCALAGGTGTCAATTTTGTGAGAAAGCGGACACGGAGAAGATGTACGCCATGAAGT	208
QY	158	ACATGAAATAAAACAAAGTGTGCTGAGAGCGCAATGAAAGTCAGAAATGTCTTCAAGGAACTCC	217
Db	209	ACATGAACAAGCAGCAGTGCATCGAGCGCGACGAGGTCCGCAACGTCTTCGGGAGCTGG	268
QY	218	AGATCATCGAGGTCTCGAGCACCCCTTTCCTGGTTAAATTTGTGTGATTTCTTCCAAAGT	277
Db	269	AGATCTTCGAGGAGATCGAGCAAGTCTTCCTGGTGAACCTCTGGTACTCTCTTCCAGGACG	328
QY	278	AGGAAGACATGTTTCATCGTGGTGAGACCTCTCTGCTGGGTGGAGACCTCGCTTATCACCTGC	337
Db	329	AGGAGGACATGTTTCATGGTCTGGACCTGCTACTGGCGGGGACCTGGCTACCACTCTGC	388
QY	338	AACAGAACGTCCACTTCAAGGAAGAAACAGTGAAGCTCTTTCATCTGTGAGCTGGTCAATGG	397
Db	389	AGCAGAACGTGCAGTTCTCCGAGGACACGGTAGGCTGTACATCTGGCGGAGCTGGCTACCTGG	448
QY	398	CCCTGGACTACCTTCAGAAACAGCGGCATCATTCACAGGGATATGAAGCCCTGACAAATTTT	457
Db	449	CTCTGGACTACTTGGCGGGCAGACACATCATCCAGAGATGTCAAGCCCTGACAACTTC	508
QY	458	TACTTGACGAACATGGGCACGTGCATCAAGATTTCAACATTTGCTGCGATGCTGCCCA	517
Db	509	TCCTGGATGAGAGAGACATGCACACCTGACCGACTTCAACATTTGCCACCATCATCAAGG	568
QY	518	GGGAGACACAGATTACCAACATGGTGGCACAGCCCTTACATGGCACTTGAGATTTCA	577
Db	569	ACGGGAGCGGGCGACGGCATTAGCAGGCCACCAAGCCGTACATGGCTCCGGAGATCTTCC	628
QY	578	GCTC-----CAGAAAAGCAGAGGCTATTCTTTTGTGTGTGACTGGTGTGCTCCTGGGAG	631
Db	629	ACTCTTTTGTCAACGGCGGACCGGCTACTCTCTTCGAGGTGGAATGTTGGTTCGGTGGGG	688
QY	632	TGACGGCATATGAATCTGTGAGAGCGCGGAGACCGTATCATATTCGCTCCAGTACTTTCCA	691
Db	689	TGATGGCCTATGAGCTGCTCGAGGATGAGAGGCCCTATGCATATCCATCCAGCAACGCCG	748
QY	692	GCAAGGAAATTGATACACGTTTTGAGACGACTGTGTAACTTACCTTCTGCTGGTGTAC	751
Db	749	TGGAGTCCCTGGTGCAGCTGTTTCAGCACCGTGAGCGTCCAGTATGTCCCCACATGGTCCA	808
QY	752	AGGAATGTGTCACTTCTTAAAGACTACTCGAACTTAATCCAGAGCCACGATTTTCTC	811

RESULT 12

Db	809	AGGAGATGGTGGCCCTTCTGCTGGGAAGACTCTCTACTGTGAACCCCGAGCACCGGCTCTCCA	868
QY	812	AGTTATCTGATGTCAGAACTTCCCGTATATGAATATAAACTCGGATGCGAGTTTTTC	871
Db	869	GCCTCCAGGACGTGACGAGCCCGCGCTGCGCGCGTGTGTGGACCACTGAGCG	928
QY	872	AGAGAGGCTCAITTCAGGTTTCAATCTCTAATAAAGCAGGCTGAATTGTGATCCTACCT	931
Db	929	AGAAGAGGTTGGAGCCGGGCTTCGTGCCCAACAAAGGCGCTGTGCACCTCGACCCACCT	988
QY	932	TTGAACCTTGAGGAATGATTTTGGAGTCCAAACCTCTACATAGAAAAAAGCGCTCTGG	991
Db	989	TTGAGCTGGAGGAGATCATCTGTGAGTCCAGGCCCTTCACAAGAAAGAAAGCGCGCTGG	1048
QY	992	CAAAAGAAAGGA-----GAAGGATATGAGGAAATGCGAATCTTCTCAGACATGTCTCTTTC	1045
Db	1049	CCAAGAACAGTCCCGGACAAACAGCAGGACAGCTCCCGAGTCCGAGATGACTATCTTC	1108
QY	1046	AAGAGCACCCTGACTCTGTCCAGAAGAGTTCAATAATTTTCAACAGAGAAAAAGTAAACA	1105
Db	1109	AAGACTCGCTCGATCGCAATCCAGCAAGACTTCGTGATTTTTTAAACAGAGAAAAAGCTGAAGA	1168
QY	1106	GG 1107	
Db	1169	GG 1170	

RESULT 11

US-09-801-876B-3

; Sequence 3, Application US/09801876B

; Patent No. 6492155

; GENERAL INFORMATION:

; APPLICANT: YE, Jane et al

; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: CL001160

; CURRENT APPLICATION NUMBER: US/09/801,876B

; CURRENT FILING DATE: 2001-03-09

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 148567

; TYPE: DNA

; ORGANISM: Human

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)...(148567)

; OTHER INFORMATION: n = A,T,C or G

US-09-801-876B-3

Query Match	14.9%;	Score 181.8;	DB 4;	Length 148567;
Best Local Similarity	89.9%;	Pred.No. 2.8e-47;		
Matches 195;	Conservative 0;	Mismatches 22;	Indels 0;	Gaps 0;
Qy	252	TAATTTGTGATATTCCTTCCAAAGATCAGGAAGACATGTTCTATGGTGGTGGACCTCCTGCT	311	
Db	86036	TAATTCAGGTATTCCTTCCAAAGATGAGGAGACATGTTCTATGGTGGTGGACCTCCTGCT		
Qy	312	GGGTGGAGACCTGCGTTATCATCCTGCAACAGAAAGTCCACTTCAAGGAAGAAACAGTGAA	371	
Db	86096	GGGTGGAGACCTGCGTTATCATCCTGCAACAGAAAGTCCACTTCAAGGAAGAAACAGTGAA		
Qy	372	GCCTTCATCTGTGAGCTGGTGCATGGCCCTGGACCTACCTGCAGACACGAGCCATCATCA	431	
Db	86156	GCCTTCATCTGTGAGCTGGTGCATGGCCCTGGACCTACCTGCAGACACGAGCCATCATCA		
Qy	432	CAGGGATATGAAGCCCTGACAAATATTTTACTTGAAGAA	468	
Db	86216	CAGGTCAAGTCAAGTCCAAAGGAGATGGCCATGAACGTA	86252	

RESULT 12


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QY 112 TGCATTGTACAGAGAATGATACCAAGAAGATGTACGCAATGAAGTACATGAATAAACAA 171
Db 255 ATGCTGGTGAACACACAGGAGACCGGGAACCACTATGCCATGAAGATCCTCGACAAACAG 314
QY 172 AAGTCGCTGGAGCGCAATGAAGTGAAGAAATGTCTTCAAGGAACCTCCAGATCATGCGAGGT 231
Db 315 AAGTGGTGAACCTGAACACAGATCGAACACACACCCCTGAAATGAAGACGATCCTGCAAGCT 374
QY 232 CTGGAGCACCTTCTCTGTTAAATTTGTTGTTATTCCTTCAAGATGAGGAAGACATGTTTC 291
Db 375 GTCAACTTTCGTTCTCGTCAACTCGAGTTCTCTTCAAGGACAACTCAAACTTATAC 434
QY 292 ATGTTGGTGACCTCTCTGCTGGGTGAGACCTGCGTTATCACTTGCACAGAACGTCAC 351
Db 435 ATGTTGATGAGTACGTCGCCGCGGGGAGATGTTCTCACACCTACGCGGATCGGAAGG 494
QY 352 TTCAAGGAAGAAACAGTGAAGCTCTTCACTGTGAGCTGGTTCATGCGCCCTGACTACCTG 411
Db 495 TTCAAGTGAAGCCATGCGCCGTTTCTACGCGGCCAGATCGTCTGACCTTTGAGTATCTG 554
QY 412 CAGAACACGCGCATCATTCACAGGATATGAAGCCTGACAAATATTTTACTTTGACGAACAT 471
Db 555 CACTCGCTGGATCTCATCTACAGGACCTGAAGCCGGAGATCTGCTCATTTGACCGAG 614
QY 472 GGGCAGTGCATCAGATATTCACATTTGCTGCGATGCTGCCAGGGAGACACAGATT 531
Db 615 GGCTACATTCAGGTGACAGACTTCGGTTTCGCCAA-----GCGCGTGAAGGCGGCACT 668
QY 532 ACCACATGGCTGGACCAAGCTTACATGGCACTGAGATGTTTCAGCTCCAGAAAGGA 591
Db 669 TGGACCTTGTGCGGACCCCTGAGTACCTGCGCCCTGAGATTATCTGAGCAA----- 721
QY 592 GCAGGCTATTCTTTGCTGTTGACTGGTGGTCCCTGGGAGTGACGGCATATGAACCTG 648
Db 722 --AGGCTACAAACAGGCGGTGAGTGGTGGGCTTGGGGTCTTATCTATGAATG 776
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RESULT 15

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US-09-394-455-5
; Sequence 5, Application US/09394455
; Patent No. 6531305
; GENERAL INFORMATION:
; APPLICANT: Witman, George F.
; APPLICANT: San Agustin, Jovenal
; APPLICANT: Leszyk, John D.
; TITLE OF INVENTION: SPERM ASSOCIATED PROTEIN KINASE POLYPEPTIDES, CORRESPONDING
; TITLE OF INVENTION: NUCLEIC ACIDS, AND METHODS OF USE
; FILE REFERENCE: 07917/078001
; CURRENT APPLICATION NUMBER: US/09/394,455
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 60/099,771
; PRIOR FILING DATE: 1998-09-10
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2549
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (81)...(1133)
; NAME/KEY: misc feature
; LOCATION: (1)...(2549)
; OTHER INFORMATION: n = A,T,C or G
US-09-394-455-5
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Query Match 11.0%; Score 134.2; DB 4; Length 2549;
Best Local Similarity 54.3%; Pred. No. 5.3e-33;
Matches 324; Conservative 0; Mismatches 258; Indels 15; Gaps 2;
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QY 52 GTCAACTTTGACCACTTTGAAATTTTGGAGCCATGGGAAGGAGGATTTGGGAAGGTC 111
Db 195 GCCCACTTGGATCAGTTTGAACGAATCAAGACCTTCGACGGGCTCCTTCGGGCGGGTG 254
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QY 112 TGCATTGTACAGAGAATGATACCAAGAAGATGTACGCAATGAAGTACATGAATAAACAA 171
Db 255 ATGCTGGTGAACACACAGGAGACCGGGAACCACTATGCCATGAAGATCCTCGACAAACAG 314
QY 172 AAGTCGCTGGAGCGCAATGAAGTGAAGAAATGTCTTCAAGGAACCTCCAGATCATGCGAGGT 231
Db 315 AAGTGGTGAACCTGAACACAGATCGAACACACACCCCTGAAATGAAGACGATCCTGCAAGCT 374
QY 232 CTGGAGCACCTTCTCTGTTAAATTTGTTGTTATTCCTTCAAGATGAGGAAGACATGTTTC 291
Db 375 GTCAACTTTCGTTCTCGTCAACTCGAGTTCTCTTCAAGGACAACTCAAACTTATAC 434
QY 292 ATGTTGGTGACCTCTCTGCTGGGTGAGACCTGCGTTATCACTTGCACAGAACGTCAC 351
Db 435 ATGTTGATGAGTACGTCGCCGCGGGGAGATGTTCTCACACCTACGCGGATCGGAAGG 494
QY 352 TTCAAGGAAGAAACAGTGAAGCTCTTCACTGTGAGCTGGTTCATGCGCCCTGACTACCTG 411
Db 495 TTCAAGTGAAGCCATGCGCCGTTTCTACGCGGCCAGATCGTCTGACCTTTGAGTATCTG 554
QY 412 CAGAACACGCGCATCATTCACAGGATATGAAGCCTGACAAATATTTTACTTTGACGAACAT 471
Db 555 CACTCGCTGGATCTCATCTACAGGACCTGAAGCCGGAGATCTGCTCATTTGACCGAG 614
QY 472 GGGCAGTGCATCAGATATTCACATTTGCTGCGATGCTGCCAGGGAGACACAGATT 531
Db 615 GGCTACATTCAGGTGACAGACTTCGGTTTCGCCAA-----GCGCGTGAAGGCGGCACT 668
QY 532 ACCACATGGCTGGACCAAGCTTACATGGCACTGAGATGTTTCAGCTCCAGAAAGGA 591
Db 669 TGGACCTTGTGCGGACCCCTGAGTACCTGCGCCCTGAGATTATCTGAGCAA----- 721
QY 592 GCAGGCTATTCTTTGCTGTTGACTGGTGGTCCCTGGGAGTGACGGCATATGAACCTG 648
Db 722 --AGGCTACAAACAGGCGGTGAGTGGTGGGCTTGGGGTCTTATCTATGAATG 776
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Search completed: December 20, 2004, 06:43:28

Job time : 94 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 20, 2004, 02:02:51 ; Search time 468 Seconds
(without alignments)

13729.255 Million cell updates/sec

Title: US-10-620-845-8

Perfect score: 1224

Sequence: 1 atgggagccacacttcaag.....agacctgaaagtctcataa 1224

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq 23Sep04:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001s:*
- 5: Geneseq2001bs:*
- 6: Geneseq2002as:*
- 7: Geneseq2002bs:*
- 8: Geneseq2003as:*
- 9: Geneseq2003bs:*
- 10: Geneseq2003cs:*
- 11: Geneseq2003ds:*
- 12: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1224	100.0	1224	6	AAD23678
2	1224	100.0	1675	6	AAD23680
3	1165.4	95.2	1191	6	AAD23679
4	1165.4	95.2	1594	4	AAD46891
5	1165.4	95.2	1594	6	AAD34317
6	1163.8	95.1	1191	12	ADL27078
7	1163.8	95.1	1281	6	AAI70704
8	1163.8	95.1	1281	12	ADL27076
9	1160.6	94.8	1485	9	ACA62840
10	1160.6	94.8	1485	10	ABS55499
11	1160.6	94.8	1485	12	ADL09161
12	1032.2	84.3	2063	11	ADM01546
13	948.6	77.5	2477	10	ADF44501
14	948.6	77.5	3766	10	ADF44497
15	832.8	68.0	981	4	AS06704
16	672.8	55.0	678	4	ASA08463
17	661	54.0	711	6	AD23677
18	660	53.9	678	6	AAD23676
19	542.4	44.3	1587	6	ABQ61051
20	542.4	44.3	3224	4	AAF44625
21	542.4	44.3	3224	10	ADE38374

22	542.4	44.3	3224	10	ADA19317	Ada19317 Human ins
23	542.4	44.3	3224	10	ACC72764	Acc72764 Human can
24	542.4	44.3	3224	12	ADI29323	Adi29323 Human MAR
25	542.4	44.3	3224	12	ADP07325	Adp07325 Human HSA
26	542.4	44.3	3224	12	ADQ17597	Adq17597 Human sof
27	519.6	42.5	3244	4	AAS46210	Aas46210 Human DNA
28	519.6	42.5	3244	8	ACA89660	Aca89660 cDNA enco
29	519.6	42.5	3244	8	ACA73670	Aca73670 Human sec
30	519.6	42.5	3244	8	ACA05985	Aca05985 Human sec
31	519.6	42.5	3244	8	ACA66819	Aca66819 cDNA enco
32	519.6	42.5	3244	8	ACF20394	Acf20394 Human sec
33	519.6	42.5	3244	8	ACF19780	Acf19780 Human sec
34	519.6	42.5	3244	8	ACD22068	Acd22068 Human sec
35	519.6	42.5	3244	8	ACF13233	Acf13233 Human sec
36	519.6	42.5	3244	8	ACD25336	Acd25336 Human sec
37	519.6	42.5	3244	8	ACF00385	Acf00385 Human sec
38	519.6	42.5	3244	8	ACA72442	AcA72442 Novel hum
39	519.6	42.5	3244	8	ACD04966	Acd04966 Novel hum
40	519.6	42.5	3244	8	ACD18427	Acd18427 Human sec
41	519.6	42.5	3244	8	ACD08434	Acd08434 Human sec
42	519.6	42.5	3244	8	ACA88868	Aca88868 Novel hum
43	519.6	42.5	3244	8	ACA70310	AcA70310 Human sec
44	519.6	42.5	3244	8	ACD12532	Acd12532 Novel hum
45	519.6	42.5	3244	8	ACC74447	Acc74447 Human sec

ALIGNMENTS

RESULT 1

AAD23678
ID AAD23678 standard; cDNA; 1224 BP.

XX AAD23678;

DT 07-MAR-2002 (first entry)

DE Novel human protein (NHP) kinase cDNA #3.

XX Novel human protein; NHP; gene therapy; diagnosis; drug screening;
KW gene expression; breast cancer; prostate cancer; nutraceutical; cosmetic;
KW medical disorder; mental; biological; physiological; chemotherapeutic;
KW ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..1224

FT /*tag= a

FT /product= "Novel human protein (NHP) kinase"

XX WO200181557-A2.

XX PN

XX PD

XX PD

XX PF

XX PF

XX PR

XX PR

XX PR

XX PA

XX PA

XX PI

XX PI

XX DR

XX DR

XX DR

XX DR

XX PT

XX PT

XX PT

XX PT

XX PT

XX PT

XX PT

XX PT

XX PT

XX PT

Hu Y, Nepomniichy B, Wang X, Donoho G, Scoville J, Walke DW;

WPI; 2002-034442/04.

P-PSDB; AAE14260.

New nucleic acid molecules encoding new human proteins, useful in diagnosis, drug screening, clinical trial monitoring, treatment of physiological disorders, and cosmetic or nutraceutical applications.

Claim 4; Page 41; 44pp; English.

Tue Dec 21 14:31:33 2004

The invention relates to novel human protein (NHP) kinases and their corresponding cDNA molecules. NHP kinase and its DNA are useful as reagents in assays for screening compounds that can be used as pharmaceutical reagents useful in the therapeutic treatment of mental, biological and medical disorders, and also as chemotherapeutic agents useful in the treatment of breast cancer and prostate cancer. NHP DNA is useful for diagnosis, drug screening, clinical trial monitoring, and useful for diagnosis, drug screening, clinical trial monitoring, and treatment of physiological disorders or diseases, and cosmetic and nutraceutical applications. NHP DNA is also useful for the identification of coding sequence and the mapping of a unique gene to a particular chromosome. NHP DNA is further useful as hybridisation probes for screening libraries and assessing gene expression patterns, and also for the detection of mutant NHPs or inappropriately expressed NHPs for disease diagnosis. NHP DNA is also useful in gene therapy. The present sequence is novel human protein (NHP) kinase cDNA which is similar to serine/threonine protein kinases, ribosomal protein kinases and cAMP-dependent kinases cDNA related to the invention

SQ Sequence 1224 BP; 381 A; 263 C; 283 G; 297 T; 0 U; 0 Other;

Query Match 100.0%; Score 1224; DB 6; Length 1224;

Best Local Similarity 100.0%; Pred No. 0;

Matches 1224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAGGCAACACTTCAAGAAACACCGAGTGTGATGAAATGAAGATGTCAACTTT 60

DB 1 ATGGAGGCAACACTTCAAGAAACACCGAGTGTGATGAAATGAAGATGTCAACTTT 60

QY 61 GACCACTTTGAAATTTTCGAGCCATTGGGAAGGCGATTTTGGGAGTCTGCATTGTA 120

DB 61 GACCACTTTGAAATTTTCGAGCCATTGGGAAGGCGATTTTGGGAGTCTGCATTGTA 120

QY 121 CAGAAATGATACCAAGAAAGATGACCAATGAAGTACATGATTAACAAAGTGCCTG 180

DB 121 CAGAAATGATACCAAGAAAGATGACCAATGAAGTACATGATTAACAAAGTGCCTG 180

QY 181 GAGCGCATGATGAGAAATGCTTCAAGGAATCTCCAGATCATGCGAGTCTGGAGCAC 240

DB 181 GAGCGCATGATGAGAAATGCTTCAAGGAATCTCCAGATCATGCGAGTCTGGAGCAC 240

QY 241 CCTTCTCTGGTTAATTTGGTGTATCTTCAAGATGAGGAGACATGTTCAATGTTGGT 300

DB 241 CCTTCTCTGGTTAATTTGGTGTATCTTCAAGATGAGGAGACATGTTCAATGTTGGT 300

QY 301 GACCTCTGCTGGTGGAGACCTGCGTTATCACCTCAACAGAACTCCACTTCAAGGAA 360

DB 301 GACCTCTGCTGGTGGAGACCTGCGTTATCACCTCAACAGAACTCCACTTCAAGGAA 360

QY 361 GAAACAGTGAAGCTTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420

DB 361 GAAACAGTGAAGCTTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420

QY 421 CGCATCATTCACAGGATATGAAGCTGCAATTTTACCTGCAAGCAATGGGACCGTG 480

DB 421 CGCATCATTCACAGGATATGAAGCTGCAATTTTACCTGCAAGCAATGGGACCGTG 480

QY 481 CACATCACAGATTTCAACATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540

DB 481 CACATCACAGATTTCAACATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540

QY 541 GCTGGCAACAGCTTACATGCGACCTGAGTGTTCAGTCCAGAAAGGAGCGAGGTAT 600

DB 541 GCTGGCAACAGCTTACATGCGACCTGAGTGTTCAGTCCAGAAAGGAGCGAGGTAT 600

QY 601 TCCTTTGCTGTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660

DB 601 TCCTTTGCTGTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660

QY 661 AGACCGGTATCATTTTCGCTCAGTACCTTCCAGCAAGCAATTTGATACACGTTGAG 720

DB 661 AGACCGGTATCATTTTCGCTCAGTACCTTCCAGCAAGCAATTTGATACACGTTGAG 720

QY 721 ACTGTGTAACTTACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780

Db 721 ACTGTGTAACTTACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780

QY 781 CTGGAACCTAATCCAGACCAAGATTTTCTAGTTATCTGATGTCAGAAATCTCCCGTAT 840

Db 781 CTGGAACCTAATCCAGACCAAGATTTTCTAGTTATCTGATGTCAGAAATCTCCCGTAT 840

QY 841 ATGAATGATATAACTGGGATGAGTGTTCAGAGAGGCTCATTCAGGTTTCAATCT 900

Db 841 ATGAATGATATAACTGGGATGAGTGTTCAGAGAGGCTCATTCAGGTTTCAATCT 900

QY 901 ATAAAGGCGAGCTGAATTTGATGTCCTTAACTTGAAGTGAAGTGAAGTGAAGTGA 960

Db 901 ATAAAGGCGAGCTGAATTTGATGTCCTTAACTTGAAGTGAAGTGAAGTGAAGTGA 960

QY 961 AAACCTCTACATAGAAAAAAGCGTCTGCAAGAGGAGGATATGAGGAATGC 1020

Db 961 AAACCTCTACATAGAAAAAAGCGTCTGCAAGAGGAGGATATGAGGAATGC 1020

QY 1021 GATTTCTTCTCAGACATGCTTCTTCAAGGACCTTCACTCTGTCAGAAAGGATTCATA 1080

Db 1021 GATTTCTTCTCAGACATGCTTCTTCAAGGACCTTCACTCTGTCAGAAAGGATTCATA 1080

QY 1081 ATTTTCAACAGAAAAAGTAAACAGGAGCTTTTAAACAAACCAACCAATCTAGCCTTG 1140

Db 1081 ATTTTCAACAGAAAAAGTAAACAGGAGCTTTTAAACAAACCAACCAATCTAGCCTTG 1140

QY 1141 GAAACAAACCAAGACCCCAAGTGAACAAATGGACAAATGGACAAATGGACAAATGG 1200

Db 1141 GAAACAAACCAAGACCCCAAGTGAACAAATGGACAAATGGACAAATGGACAAATGG 1200

QY 1201 TTTTCAAGCTTCAAGAGTTTCATA 1224

Db 1201 TTTTCAAGCTTCAAGAGTTTCATA 1224

RESULT 2

AD23680

ID AD23680 standard; DNA; 1675 BP.

XX

AC AD23680;

XX

DT

XX

07-MAR-2002 (first entry)

XX

Novel human protein (NHP) kinase full-length ORF and flanking region DNA.

XX

Novel human protein; NHP; gene therapy; diagnosis; drug screening;

XX

gene expression; breast cancer; prostate cancer; nutraceutical; cosmetic;

XX

medical disorder; mental; biological; physiological; chemotherapeutic;

XX

ds.

XX

Homo sapiens.

XX

WO200181557-A2.

XX

01-NOV-2001.

XX

24-APR-2001; 2001WO-US013149.

XX

25-APR-2000; 2000US-0199499P.

XX

01-MAY-2000; 2000US-0201227P.

XX

(LEXI-) LEXICON GENETICS INC.

XX

Hu Y, Nepomnichy B, Wang X, Donoho G, Scoville J, Walke DW;

XX

WPI; 2002-034442/04.

XX

New nucleic acid molecules encoding new human proteins, useful in

XX

PT diagnosis, drug screening, clinical trial monitoring, treatment of

XX

PT physiological disorders, and cosmetic or nutraceutical applications.

XX

Disclosure; Page 44; 44pp; English.

PS

XX CC The invention relates to novel human protein (NHP) kinases and their
 CC corresponding cDNA molecules. NHP kinase and its DNA are useful as
 CC reagents in assays for screening compounds that can be used as
 CC pharmaceutical reagents useful in the therapeutic treatment of mental,
 CC biological and medical disorders, and also as chemotherapeutic agents
 CC useful in the treatment of breast cancer and prostate cancer. NHP DNA is
 CC useful for diagnosis, drug screening, clinical trial monitoring, the
 CC treatment of physiological disorders or diseases, and cosmetic and
 CC nutraceutical applications. NHP DNA is also useful for the identification
 CC of coding sequence and the mapping of a unique gene to a particular
 CC chromosome. NHP DNA is further useful as hybridisation probes for
 CC screening libraries and assessing gene expression patterns, and also for
 CC the detection of mutant NHPs or inappropriately expressed NHPs for
 CC disease diagnosis. NHP DNA is also useful in gene therapy. The present
 CC sequence is novel human protein (NHP) kinase full-length ORF (open
 CC reading frame) and flanking region DNA related to the invention
 XX SQ Sequence 1675 BP; 469 A; 404 C; 414 G; 388 T; 0 U; 0 Other;

Query Match 100.0%; Score 1224; DB 6; Length 1675;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGAGCCAACTTCAAGAAACCCACGCTGTTTGTATGAATGAAGATGTCAACTTT 60
 DB 413 ATGGGAGCCAACTTCAAGAAACCCACGCTGTTTGTATGAATGAAGATGTCAACTTT 472

QY 61 GACCACCTTTGAAATTTTGCAGGCCATTGGGAAAGCCAGTTTGGGAAAGTCTGCAATTGTA 120
 DB 473 GACCACCTTTGAAATTTTGCAGGCCATTGGGAAAGCCAGTTTGGGAAAGTCTGCAATTGTA 532

QY 121 CAGAAGAATGATACCAAGAAGATGACCAATGAAGTACATGAATAAACAAGTGGCGTG 180
 DB 533 CAGAAGAATGATACCAAGAAGATGACCAATGAAGTACATGAATAAACAAGTGGCGTG 592

QY 181 GAGCGCAATGAAGTGAGAAATGCTTCAAGAACTCCAGATCATGCGGGTCTCGAGCAC 240
 DB 593 GAGCGCAATGAAGTGAGAAATGCTTCAAGAACTCCAGATCATGCGGGTCTCGAGCAC 652

QY 241 CCTTTCCTGGTTAATTTGTGGTATTCTTCAAGATGAGGAAGACATGTTTCATGGTGTG 300
 DB 653 CCTTTCCTGGTTAATTTGTGGTATTCTTCAAGATGAGGAAGACATGTTTCATGGTGTG 712

QY 301 GACCTCTGCTGGTGGAGACCTGGTTATCACTGCAACAGACGTCCTCAAGGAA 360
 DB 713 GACCTCTGCTGGTGGAGACCTGGTTATCACTGCAACAGACGTCCTCAAGGAA 772

QY 361 GAAACAGTGAAGCTTTCATCTGTGAGCTGTGCTGATGCGCCCTGGACTACCTGCAGACCAG 420
 DB 773 GAAACAGTGAAGCTTTCATCTGTGAGCTGTGCTGATGCGCCCTGGACTACCTGCAGACCAG 832

QY 421 CGCATCTTCAAGGATATGAAGCTCACAATATTTTACTTTGAGCAATCGGCAGCTG 480
 DB 833 CGCATCTTCAAGGATATGAAGCTCACAATATTTTACTTTGAGCAATCGGCAGCTG 892

QY 481 CACATCAGAGATTTCACATCTGCTGATGCTGCCAGGGAGACACAGATTACCAACCATG 540
 DB 893 CACATCAGAGATTTCACATCTGCTGATGCTGCCAGGGAGACACAGATTACCAACCATG 952

QY 541 GCTGGCACCAGCCTTACATGCGCACCCTGAGATGTTTCAGCTCCAGAAAGGAGCAGCTAT 600
 DB 953 GCTGGCACCAGCCTTACATGCGCACCCTGAGATGTTTTCAGCTCCAGAAAGGAGCAGCTAT 1012

QY 601 TCCTTTGCTGTGACTGTGGTCCCTGGAGTGAGCGCATATGAATCTGCTGAGAGCGCG 660
 DB 1013 TCCTTTGCTGTGACTGTGGTCCCTGGAGTGAGCGCATATGAATCTGCTGAGAGCGCG 1072

QY 661 AGACCGTATCATATTTCGCTCCAGTACTTCCAGCAAGGAAATTTGTACACAGCTTTGAGACG 720
 DB 1073 AGACCGTATCATATTTCGCTCCAGTACTTCCAGCAAGGAAATTTGTACACAGCTTTGAGACG 1132

QY 721 ACTGTTGTAACCTTACCCCTTCTGCGCTGGTGCACAGGAAATGGTGTCACTCTTTAAAGGCTA 780

DB 1133 ACTGTTGTAACCTTACCCCTTCTGCGCTGTCACAGGAAATGGTGTCACTCTTTAAAGGCTA 1192
 QY 781 CTGGAACCTTAATCCAGACCAACGATTTTCTCAGTTATCTGATGTCCAGAACTTCCCGTAT 840
 DB 1193 CTGGAACCTTAATCCAGACCAACGATTTTCTCAGTTATCTGATGTCCAGAACTTCCCGTAT 1252
 QY 841 ATGAATCATATAAAGCTGGGATGCAAGTTTTCAGAAAGAGGCTCATTTCCAGGTTTTCATTCCT 900
 DB 1253 ATGAATCATATAAAGCTGGGATGCAAGTTTTCAGAAAGAGGCTCATTTCCAGGTTTTCATTCCT 1312
 QY 901 AATAAAGCGCAGGCTGAATTTGTGATCTCTACCTTTGAACTTGAGGAAATGATTTTGGAGTCC 960
 DB 1313 AATAAAGCGCAGGCTGAATTTGTGATCTCTACCTTTGAACTTGAGGAAATGATTTTGGAGTCC 1372
 QY 961 AAACCTCTACATAGAAGAAAAAGCGCTCTGGCAAGAGGAGGAGATATGAGGAAATGC 1020
 DB 1373 AAACCTCTACATAGAAGAAAAAGCGCTCTGGCAAGAGGAGGAGATATGAGGAAATGC 1432
 QY 1021 GATTTCTTCTCAGACATGCTCTTCTTCAAGAGCACCCTTGACTCTGTCCAGAGGAGTTCATA 1080
 DB 1433 GATTTCTTCTCAGACATGCTCTTCTTCAAGAGCACCCTTGACTCTGTCCAGAGGAGTTCATA 1492
 QY 1081 ATTTTCAACAGAGAAAAAGTAAACAGGGAATTTTAAACAAAAGACAAACCAATCTAGCCCTTG 1140
 DB 1493 ATTTTCAACAGAGAAAAAGTAAACAGGGAATTTTAAACAAAAGACAAACCAATCTAGCCCTTG 1552
 QY 1141 GAACAAACCAAGACCCACAGTGACAAATGGACAAATGGACACAGGACTCAGTGAGACT 1200
 DB 1553 GAACAAACCAAGACCCACAGTGACAAATGGACAAATGGACACAGGACTCAGTGAGACT 1612
 QY 1201 TTTTCAGACCTCGAAGTTTTCATA 1224
 DB 1613 TTTTCAGACCTCGAAGTTTTCATA 1636

RESULT 3
 AAD23679
 ID AAD23679 standard; cDNA; 1191 BP.
 XX AC AAD23679;
 DT 07-MAR-2002 (first entry)
 XX DE Novel human protein (NHP) kinase cDNA #4.
 DE Novel human protein; NHP; gene therapy; diagnosis; drug screening;
 KW gene expression; breast cancer; prostate cancer; nutraceutical; cosmetic;
 KW medical disorder; mental; biological; physiological; chemotherapeutic;
 KW ss.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers.
 FT CDS 1..1191
 FT /*tag= a
 FT /product= "Novel human protein (NHP) kinase"
 XX PN WO200181557-A2.
 XX PD 01-NOV-2001.
 XX PF 24-APR-2001; 2001WO-US013149.
 XX PR 25-APR-2000; 2000US-0199499P.
 XX PR 01-MAY-2000; 2000US-0201227P.
 XX PA (LEXI-) LEXICON GENETICS INC.
 XX PI Hu Y, Nepomnichy B, Wang X, Donoho G, Scoville J, Walke DW;
 XX WPI; 2002-034442/04.
 DR P-FSDB; AAE14261.

XX New nucleic acid molecules encoding new human proteins, useful in
PT diagnosis, drug screening, clinical trial monitoring, treatment of
PT physiological disorders, and cosmetic or nutraceutical applications.
XX Claim 7; Page 42; 44pp; English.

XX The invention relates to novel human protein (NHP) kinases and their
CC corresponding cDNA molecules. NHP kinase and its DNA are useful as
CC reagents in assays for screening compounds that can be used as
CC pharmaceutical reagents useful in the therapeutic treatment of mental,
CC biological and medical disorders, and also as chemotherapeutic agents
CC useful in the treatment of breast cancer and prostate cancer. NHP DNA is
CC useful for diagnosis, drug screening, clinical trial monitoring, the
CC treatment of physiological disorders or diseases, and cosmetic and
CC nutraceutical applications. NHP DNA is also useful for the identification
CC of coding sequence and the mapping of a unique gene to a particular
CC chromosome. NHP DNA is further useful as hybridisation probes for
CC screening libraries and assessing gene expression patterns, and also for
CC the detection of mutant NHPs or inappropriately expressed NHPs for
CC disease diagnosis. NHP DNA is also useful in gene therapy. The present
CC sequence is novel human protein (NHP) kinase cDNA which is similar to
CC serine/threonine protein kinases, ribosomal protein kinases and CAMP-
CC dependent kinases cDNA related to the invention

XX Sequence 1191 BP; 369 A; 254 C; 278 G; 290 T; 0 U; 0 Other;

Query Match 95.2%; Score 1165.4; DB 6; Length 1191;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 1172; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 ATGGAGGCCAACACCTTCAAGAAACACACAGTGTGTTGATGAATGAAGATGTCAACTTT 60
DB 1 ATGGAGGCCAACACCTTCAAGAAACACACAGTGTGTTGATGAATGAAGATGTCAACTTT 60

QY 61 GACCACTTTGAAATTTGGAGCCATTTGGAAAGCCAGTTTGGAGAGTCTGCATTTGTA 120
DB 61 GACCACTTTGAAATTTGGAGCCATTTGGAAAGCCAGTTTGGAGAGTCTGCATTTGTA 120

QY 121 CAGAAGATGATACCAAGAGATGTACCAATGAATGATGATGATGATGATGATGATGATG 180
DB 121 CAGAAGATGATACCAAGAGATGTACCAATGAATGATGATGATGATGATGATGATGATG 180

QY 181 GAGCGCAATGAAGTGAAGATGTCTTCAAGAACTCCAGATCATCGAGGCTCGAGCAC 240
DB 181 GAGCGCAATGAAGTGAAGATGTCTTCAAGAACTCCAGATCATCGAGGCTCGAGCAC 240

QY 241 CCTTTCCTGGTTAATTTGGTATTTCCCTTCAAGATGAGGAGATGTTTCAATGTTGTTG 300
DB 241 CCTTTCCTGGTTAATTTGGTATTTCCCTTCAAGATGAGGAGATGTTTCAATGTTGTTG 300

QY 301 GACCTCTCTGGTGGAGACTGGTATACCTGCAACAGAGAGTCCACTTCAAGGAA 360
DB 301 GACCTCTCTGGTGGAGACTGGTATACCTGCAACAGAGAGTCCACTTCAAGGAA 360

QY 361 GAAACAGTGAAGCTCTTCATCTGTGAGTGTGTCATGGCCCTGGACTACCTGCAGAACCCAG 420
DB 361 GAAACAGTGAAGCTCTTCATCTGTGAGTGTGTCATGGCCCTGGACTACCTGCAGAACCCAG 420

QY 421 CGCATCTTACAGGGATATGAGCTGACAAATATTTTACTTGACGAAATGAGGACGTTG 480
DB 421 CGCATCTTACAGGGATATGAGCTGACAAATATTTTACTTGACGAAATGAGGACGTTG 480

QY 481 CACATCAGAGATTTCAACATTTGCTCGATGCTGCCAGGGAGACACAGATTACCACCATG 540
DB 481 CACATCAGAGATTTCAACATTTGCTCGATGCTGCCAGGGAGACACAGATTACCACCATG 540

QY 541 GCTGGCAACCAAGCCCTTACATGGCACTGAGATGTTTCACTCCAGAAAGGAGGAGGCTAT 600
DB 541 GCTGGCAACCAAGCCCTTACATGGCACTGAGATGTTTCACTCCAGAAAGGAGGAGGCTAT 600

QY 601 TCCTTTGTCTGTTGACTGTGTTCCCTGGAGTGACGGCATATGAACTGCTGAGAGGCCGG 660
DB 601 TCCTTTGTCTGTTGACTGTGTTCCCTGGAGTGACGGCATATGAACTGCTGAGAGGCCGG 660

Db 601 TCCTTTGCTGTGATCGTGGTCCCTGGAGTGCAGCATATGAACCTGCTGAGAGGCCGG 660
QY 661 AGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTTACACACGCTTTGAGACG 720
Db 661 AGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTTACACACGCTTTGAGACG 720
QY 721 ACTGTTGTAACCTTACCCTTCTGCTGCTGCATCAGGAAATGGTGTCACTTCTTAAAGGCTA 780
Db 721 ACTGTTGTAACCTTACCCTTCTGCTGCTGCATCAGGAAATGGTGTCACTTCTTAAAGGCTA 780
QY 781 CTCGAACCTAATCAGACCAACGATTTTCTCAGTATCTATGATGTCAGAACTTCCCGTAT 840
Db 781 CTCGAACCTAATCAGACCAACGATTTTCTCAGTATCTATGATGTCAGAACTTCCCGTAT 840
QY 841 ATGAATGATATAAATCTGGGATGCACTTTTTCAGAAAGGCTCATTCAGGTTTTCATTCCT 900
Db 841 ATGAATGATATAAATCTGGGATGCACTTTTTCAGAAAGGCTCATTCAGGTTTTCATTCCT 900
QY 901 AATAAAGCGCAGGCTGAATTTGTGATCTCTTCAACCTTGAGGAAATGATTTTGGAGTCC 960
Db 901 AATAAAGCGCAGGCTGAATTTGTGATCTCTTCAACCTTGAGGAAATGATTTTGGAGTCC 960
QY 961 AAACCTCTACATAAGAAAAAAGCGTCTGGCAAGAGGAGATATGAGGAAATGC 1020
Db 961 AAACCTCTACATAAGAAAAAAGCGTCTGGCAAGAGGAGATATGAGGAAATGC 1020
QY 1021 GATTCCTTCTCAGACATGCTTCTTCAAGAGCAGCTTCTGCTCCAGAGGAGTTCATA 1080
Db 1021 GATTCCTTCTCAGACATGCTTCTTCAAGAGCAGCTTCTGCTCCAGAGGAGTTCATA 1080
QY 1081 ATTTTCAACGAGAAAAAAGTAAACAGGACTTTTAAACAAAAAGACAAACAAATCTAGCCTTG 1140
Db 1081 ATTTTCAACGAGAAAAAAGTAAACAGGACTTTTAAACAAAAAGACAAACAAATCTAGCCTTG 1140
QY 1141 GAACAAACCAAGACCCACCAAGTGACAAATGGACAAATGGACA 1183
Db 1141 GAACAAACCAAGACCCACCAAGTGAGGATGGTGTGAGGATTAACA 1183

RESULT 4
AAH46891 standard; cDNA; 1594 BP.

XX AC AAH46891;
XX AC
DT 25-SEP-2001 (first entry)
XX
DE cDNA encoding human protein kinase SGK177.
XX
KW Protein kinase; enzyme; cytostatic; nootropic; neuroprotective; human;
KW antiparkinsonian; viricide; antibacterial; antifungal; antimigraine;
KW analgesic; hypotensive; viricide; hypertensive; immunosuppressive; antiallergic;
KW antiparkinsonian; antirheumatic; antidiabetic; antihypertensive; anorectic;
KW osteoporotic; thrombolytic; antiarteriosclerotic; antidiabetic; antidiabetic;
KW vasotrophic; antidiabetic; gene therapy; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
CDS 404..1594
FT /*tag= a
FT
PN WO200155356-A2.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-US002337.
XX
PR 25-JAN-2000; 2000US-0178078P.
PR 31-JAN-2000; 2000US-0179364P.
PR 17-FEB-2000; 2000US-0183173P.
PR 17-MAR-2000; 2000US-0190162P.
PR 29-MAR-2000; 2000US-0193404P.

CDS 404..1594
 FT /*tag= a
 FT /product= "Human PKIN-20 protein"
 XX
 PN WO200218557-A2.
 XX
 PD 07-MAR-2002.
 XX
 PF 31-AUG-2001; 2001WO-US027219.
 XX
 PR 31-AUG-2000; 2000US-0229873P.
 PR 08-SEP-2000; 2000US-0231357P.
 PR 14-SEP-2000; 2000US-0232654P.
 PR 22-SEP-2000; 2000US-0234902P.
 PR 29-SEP-2000; 2000US-0236499P.
 PR 06-OCT-2000; 2000US-0238389P.
 PR 13-OCT-2000; 2000US-0240542P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Bandman O, Nguyen DB, Walia NK, Hafalia AJA, Yao MG, Gandhi AR,
 PI Gururajan R, Ding L, Patterson C, Yue H, Baughn MR, Tribouley CM,
 PI Thornton M, Elliott VS, Lu Y, Ison CH, Au-Young J, Tang YT,
 PI Azimzai Y, Burdill JD, Marcus GA, Zingler KA, Lu DAM, Lal PG,
 PI Ramkumar J, Warren BA, Kearney L, Policky JL, Thangavelu K,
 PI Burford N;
 XX
 DR WPI; 2002-329769/36.
 DR P-PSDB; ABE21725.
 XX
 PT New human kinases, useful for diagnosing, treating or preventing immune
 PT system disorders (e.g. Crohn's disease), neurological disorders (e.g.
 PT epilepsy), or cell proliferative disorders (e.g. cancers such as leukemia
 PT or lymphoma).
 XX
 PS Claim 99; Page 214; 218pp; English.
 XX
 CC The present invention relates to human kinases (PKIN) and polynucleotides
 CC encoding such proteins. PKIN sequences of the invention are useful for
 CC diagnosing, treating or preventing disorders associated with aberrant
 CC expression of PKIN, particularly immune system disorders (e.g. acquired
 CC immune deficiency syndrome (AIDS), thymic hypoplasia, Crohn's disease,
 CC anaemia, asthma), neurological disorders (e.g. epilepsy, Charcot-Marie-
 CC Tooth disease or seizures), cell proliferative disorders (e.g. cancers
 CC such as adenocarcinoma, leukaemia, lymphoma, melanoma, sarcoma),
 CC and developmental disorders (e.g. Down's syndrome). They are also used in
 CC gene therapy and protein therapy. The present sequence is a cDNA encoding
 CC human PKIN-20 protein
 XX
 SQ Sequence 1594 BP; 441 A; 386 C; 395 G; 372 T; 0 U; 0 Other;
 Query Match 95.2%; Score 1165.4; DB 6; Length 1594;
 Best Local Similarity 99.1%; Pred. No. 0;
 Matches 1172; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
 QY 1 ATGGAGGCAACACCTTCAAGAAACCCACGAGTGTGTGATGAATAAGAGAGTGTCAACTTT 60
 DB 404 ATGGAGGCAACACCTTCAAGAAACCCACGAGTGTGTGATGAATAAGAGAGTGTCAACTTT 463
 QY 61 GACCACTTTGAAATTTGGAGGCCAATGGGAAAGGCGAGTTTGGGAAAGGCTGTGCATTGTA 120
 DB 464 GACCACTTTGAAATTTGGAGGCCAATGGGAAAGGCGAGTTTGGGAAAGGCTGTGCATTGTA 523
 QY 121 CAGAGAAGATGATACCAAGAAGATGACCAATGAAGTACATGAATAAACAAGAGCGGTG 180
 DB 524 CAGAGAAGATGATACCAAGAAGATGACCAATGAAGTACATGAATAAACAAGAGCGGTG 583
 QY 181 GAGCGCAATGAGTGAAGAAATGCTTCAAGGAACCTCCAGATCATGACGGGTCTGGAGCAC 240
 DB 584 GAGCGCAATGAGTGAAGAAATGCTTCAAGGAACCTCCAGATCATGACGGGTCTGGAGCAC 643
 QY 241 CCTTTCCTGGTTAATTGTTGGTATTCCTTCCAGATGAGGAAGACATGTTCAATGGTGTG 300

Db 644 CCTTTCCTGGTTAATTGTTGGTATTCCTTCCAGATGAGGAAGACATGTTTCATGGTGTG 703
 QY 301 GACCTCTCTGCTGGGTGGAGACCTCGTTATCACCTGCAACAGAAACGCTCCACTTCAAGGAA 360
 Db 704 GACCTCTCTGCTGGGTGGAGACCTCGTTATCACCTGCAACAGAAACGCTCCACTTCAAGGAA 763
 QY 361 GAAACAGTGAAGCTCTTTCATCTGTGAGCTGTGATGGCCCTGGACTACCTCGAAGAACG 420
 Db 764 GAAACAGTGAAGCTCTTTCATCTGTGAGCTGTGATGGCCCTGGACTACCTCGAAGAACG 823
 QY 421 GGCATCATTCACAGGATATCAAGCCTGACAAATATTTTACTTGACGACATGGGCACGTG 480
 Db 824 GGCATCATTCACAGGATATCAAGCCTGACAAATATTTTACTTGACGACATGGGCACGTG 883
 QY 481 CACATCAAGATTTCAACATTTGCTGCGATGCTGCCAGGGAGACACAGATTACCAACATG 540
 Db 884 CACATCAAGATTTCAACATTTGCTGCGATGCTGCCAGGGAGACACAGATTACCAACATG 943
 QY 541 GCTGGCAACCAAGCCTTACATGGCACTTGAGATGTTCAAGTCCAGAAAAGGAGCAGGCTAT 600
 Db 944 GCTGGCAACCAAGCCTTACATGGCACTTGAGATGTTCAAGTCCAGAAAAGGAGCAGGCTAT 1003
 QY 601 TCCTTTCTGCTGTTGACTGGTGTCCCTGGAGTGACGCATATGAATCACTGCTGAGAGGCCG 660
 Db 1004 TCCTTTCTGCTGTTGACTGGTGTCCCTGGAGTGACGCATATGAATCACTGCTGAGAGGCCG 1063
 QY 661 AGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTTGACACACATGTTGAGACG 720
 Db 1064 AGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTTGACACACATGTTGAGACG 1123
 QY 721 ACTGTTGTAATTAACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
 Db 1124 ACTGTTGTAATTAACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1183
 QY 781 CTCGAACTTAATCCAGACCAAGGAAATTTCTCAGTTATCTGATGTCGAGAACTTCCCGTAT 840
 Db 1184 CTCGAACTTAATCCAGACCAAGGAAATTTCTCAGTTATCTGATGTCGAGAACTTCCCGTAT 1243
 QY 841 ATGAATGATATAAACTGGGATGCAAGTATTTTTCAGAAAGAGGCTCATTCAGGTTTCATTCCT 900
 Db 1244 ATGAATGATATAAACTGGGATGCAAGTATTTTTCAGAAAGAGGCTCATTCAGGTTTCATTCCT 1303
 QY 901 AATAAAGCAGGCTGAATTTGATGCTTACCTTTGAACTTGAGGAAATGATTTTGGAGTCC 960
 Db 1304 AATAAAGCAGGCTGAATTTGATGCTTACCTTTGAACTTGAGGAAATGATTTTGGAGTCC 1363
 QY 961 AAACCTCTACATAAGAAAAGGCTGTCGCAAGAGGAGGAGGATATGAGGAATGC 1020
 Db 1364 AAACCTCTACATAAGAAAAGGCTGTCGCAAGAGGAGGAGGATATGAGGAATGC 1423
 QY 1021 GATTCTTCTCAGACATGCTTCTTCAAGAGCACCTTGACTCTGCTCCAGAAAGGAGTTCATA 1080
 Db 1424 GATTCTTCTCAGACATGCTTCTTCAAGAGCACCTTGACTCTGCTCCAGAAAGGAGTTCATA 1483
 QY 1081 ATTTTCAACAGAGAAAAGTAAACAGGACCTTTTAAACAAAAGACAAACCAATCTAGCCCTG 1140
 Db 1484 ATTTTCAACAGAGAAAAGTAAACAGGACCTTTTAAACAAAAGACAAACCAATCTAGCCCTG 1543
 QY 1141 GAACAAACCAAGAACCCACAGTGACAAATGGACAAATGGACA 1183
 Db 1544 GAACAAACCAAGAACCCACAGTGAGGATGGTCAGAAATAACA 1586
 RESULT 6
 ADL27078
 ID ADL27078 standard; cDNA; 1191 BP.
 XX
 AC ADL27078;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Novel human DNA molecule, 14911.
 XX

CC generate transgenic animals or knockout animals, which in turn are useful
CC in the development and screening of therapeutically useful reagents, for
CC chromosome identification, and tissue typing. This polynucleotide
CC sequence represents one of the novel human nucleic acid molecules of the
CC invention.

DB 341 GCTGGCACCAGGCCCTTACAIGGCACCTGAGATGTTCAAGCTCCAGATTAAGGAGCAGGCTAT 800

QY	601	TCCTTTGCTGTTGACTGCTGGTCCCTGGAGTGCAGGCATATGAACCTGCTGAGAGGCGG	660
Db	601	TCCTTTGCTGTTGACTGCTGGTCCCTGGAGTGCAGGCATATGAACCTGCTGAGAGGCGG	660
QY	661	AGACCGTATCATATTCGCTCCAGTACTTCACGCAAGGAAATGTGTACACACGTTTGAGACG	720
Db	661	AGACCGTATCATATTCGCTCCAGTACTTCACGCAAGGAAATGTGTACACACGTTTGAGACG	720
QY	721	ACTGTTGTAACTTACCTCTTCGCTCGGTGCACAGGAAATGGTGTCACTTCTTTAAAAAGCTA	780
Db	721	ACTGTTGTAACTTACCTCTTCGCTCGGTGCACAGGAAATGGTGTCACTTCTTTAAAAAGCTA	780
QY	781	CTCGAACCTTAATCCAGACCAACGATTTCTCAGTTATCTGATGTCCAGAACTTCCCGTAT	840
Db	781	CTCGAACCTTAATCCAGACCAACGATTTCTCAGTTATCTGATGTCCAGAACTTCCCGTAT	840
QY	841	ATGAATGATATAAACTGGGATGCAGTTTTTCAGAGAGGCTCATTCAGGTTTCATTCCT	900
Db	841	ATGAATGATATAAACTGGGATGCAGTTTTTCAGAGAGGCTCATTCAGGTTTCATTCCT	900
QY	901	AATTAAGGCGAGGCTGAAATGTGTATCCTACCTTTTGAACCTTGAGGAAATGATTTTGGAGTCC	960

Db 889 ATGAATGATATAAATCGGATGCGATTTTTCAGAGAGGCTCATTCAGGTTTCATTCCT 948
Qy 901 AATAAGCGCGCTGAATTTGATCTACCTTTGAACTTGAGGAAATGATTTTGGAGTCC 960
Db 949 AATAAGCGCGCTGAATTTGATCTACCTTTGAACTTGAGGAAATGATTTTGGAGTCC 1008
Qy 961 AAACCTTACATAGAAAAAAGCGTCTGCAAGAGGAGGATATGAGGAAATGC 1020
Db 1009 AAACCTTACATAGAAAAAAGCGTCTGCAAGAGGAGGATATGAGGAAATGC 1068
Qy 1021 GATTCCTTCTAGACATGCTCTTCTTCAAGAGCACCTTGACTCTGTCAGAGGAGTTTCATA 1080
Db 1069 GATTCCTTCTAGACATGCTCTTCTTCAAGAGCACCTTGACTCTGTCAGAGGAGTTTCATA 1128
Qy 1081 ATTTTCAACGAGAAAAAGTAAACAGGAGCTTTTAAACAAAGAACCAACCAATCTAGCCCTTG 1140
Db 1129 ATTTTCAACGAGAAAAAGTAAACAGGAGCTTTTAAACAAAGAACCAACCAATCTAGCCCTTG 1188
Qy 1141 GAACAAACCAAGAACCCACCAAGTCAAAATGCGACAAATGGACA 1183
Db 1189 GAACAAACCAAGAACCCACCAAGTGGAGATGGTCAGAAATACA 1231

RESULT 8
ADL27076
ID ADL27076 standard; DNA; 1281 BP.
XX AC ADL27076;
XX DT 20-MAY-2004 (first entry)
XX DE Novel human cDNA molecule, 14911.
XX KW 26199; 33530; 33949; 47148; 50226; 58764; 62113; 32144; 32235; 23565;
KW 13305; 14911; 86216; 25206; 8843; cytosolic; haemostatic; synecological;
KW nephrotropic; dermatological; immunosuppressive; antinflammatory;
KW hepatotropic; virucide; analgesic; vasotropic; gene therapy;
KW cellular proliferative; differentiative disorder; brain; platelet;
KW breast; colon; kidney; lung; ovarian; prostate; haematopoietic;
KW pancreatic; skeletal muscle; skin; bone metabolism; immune;
KW transgenic animal; chromosome identification; tissue typing; human; gene;
XX SS.
XX OS Homo sapiens.
XX PN US2004005664-A1.
XX PD 08-JAN-2004.
XX PF 10-APR-2003; 2003US-00410764.
XX PR 25-APR-2000; 2000US-0199391P.
PR 19-MAY-2000; 2000US-0205301P.
PR 15-JUN-2000; 2000US-0059392P.
PR 01-SEP-2000; 2000US-0229300P.
PR 05-OCT-2000; 2000US-0238054P.
PR 11-OCT-2000; 2000US-00686673.
PR 30-NOV-2000; 2000US-0250186P.
PR 16-FEB-2001; 2001US-0269440P.
PR 17-MAY-2001; 2001US-00860352.
PR 06-AUG-2001; 2001US-00924358.
PR 24-AUG-2001; 2001US-0314884P.
PR 27-SEP-2001; 2001US-00966614.
PR 29-OCT-2001; 2001US-0347815P.
PR 29-NOV-2001; 2001US-00997816.
PR 24-JAN-2002; 2002US-0351572P.
PR 15-FEB-2002; 2002US-00076535.
PR 23-AUG-2002; 2002US-00226410.
PR 25-OCT-2002; 2002US-00281094.
PR 24-JAN-2003; 2003US-00350553.
XX (MILL-) MILLENNIUM PHARM INC.

PI Meyers RE, Macbeth KJ, Curtis RAJ, Rudolph-Owen LA, Weich NS;
PI Olandt PJ, Tsai F, Kapeller-Libermann R, Carroll JM;
XX WPI; 2004-081724/08.
XX P-PSDB; ADL27077.
XX New isolated 26199, 33530, 33949, 47148, 50226, 58764, 62113, 32144,
XX 32235, 23565, 13305, 14911, 86216, 25206 or 8843 polypeptides and nucleic
XX acids, useful for diagnosing or treating cancer, autoimmune, metabolic
XX and viral diseases.
XX Claim 2; SEQ ID NO 100; 237pp; English.
XX The invention relates to novel nucleic acid molecules designated 26199,
XX 33530, 33949, 47148, 50226, 58764, 62113, 32144, 32235, 23565, 13305,
XX 14911, 86216, 25206 or 8843. The novel nucleic acid molecules and their
XX compositions have the following activities: cytostatic, haemostatic,
XX synecological, nephrotropic, dermatological, immunosuppressive,
XX antiinflammatory, hepatotropic, virucide, analgesic, and vasotropic. The
XX novel nucleic acid molecules may be used in gene therapy to treat
XX disorders. The methods and compositions of the present invention are
XX useful for the diagnosis, prevention and/or treatment of diseases or
XX conditions associated with aberrant expression or activity of the
XX polypeptides, such as a cellular proliferative and/or differentiative
XX disorder, brain disorder, platelet disorder, breast disorder, colon
XX disorder, kidney (renal) disorder, lung disorder, ovarian disorder,
XX prostate disorder, haematopoietic disorder, pancreatic disorder, skeletal
XX muscle disorder, skin (dermal) disorder, disorder associated with bone
XX metabolism, immune, e.g., inflammatory, disorder, cardiovascular
XX disorder, endotheelial cell disorder, liver disorder, viral diseases, pain
XX disorder, metabolic disorder, neurological or CNS disorder, erythroid
XX to identify other proteins or molecules involved in binding reaction, to
XX generate transgenic animals or knock-out animals, which in turn are useful
XX in the development and screening of therapeutically useful reagents, for
XX chromosome identification, and tissue typing. This polynucleotide
XX sequence represents one of the novel human nucleic acid molecules of the
XX invention.
XX Sequence 1281 BP; 392 A; 277 C; 299 G; 313 T; 0 U; 0 Other;
XX
XX Query Match 95.1%; Score 1163.8; DB 12; Length 1281;
XX Best Local Similarity 99.0%; Pred. No. 0;
XX Matches 1171; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
Qy 1 ATGGGAGCCCAACACTTCAAGAAACACACAGTGTTCATGAAATGAAGATGTCAACTTT 60
Db 49 ATGGGAGCCCAACACTTCAAGAAACACACAGTGTTCATGAAATGAAGATGTCAACTTT 108
Qy 61 GACCACTTTGAAATTTTGGAGCCATTTGGAAAGGCGAGTTTGGGAAGGTCGATTGTA 120
Db 109 GACCACTTTGAAATTTTGGAGCCATTTGGAAAGGCGAGTTTGGGAAGGTCGATTGTA 168
Qy 121 CAGAAGATGATACCAAGAGAGTGTACGCAATGAAGTACATGAATAACAAAGTGGGTG 180
Db 169 CAGAAGATGATACCAAGAGAGTGTACGCAATGAAGTACATGAATAACAAAGTGGGTG 228
Qy 181 GAGCGCAATGAAGTGAATAATGTCTTCAAGAACTCCAGATCATCGAGGGTCTGGAGCAC 240
Db 229 GAGCGCAATGAAGTGAATAATGTCTTCAAGAACTCCAGATCATCGAGGGTCTGGAGCAC 288
Qy 241 CCTTCTCTGGTTAAATTTGGTATTCTTCCAGATGAGGAGCATGTTTCATGTTGGTG 300
Db 289 CCTTCTCTGGTTAAATTTGGTATTCTTCCAGATGAGGAGCATGTTTCATGTTGGTG 348
Qy 301 GACCTCTCTGGTGGAGACCTTGGCTTATCCTGCAACAGAACGTCCTCAAGGAA 360
Db 349 GACCTCTCTGGTGGAGACCTTGGCTTATCCTGCAACAGAACGTCCTCAAGGAA 408
Qy 361 GAAACAGTGAAGCTCTTTCATCTGTGAGCTGGTATGCGCCCTGGACTACGCAACAG 420
Db 409 GAAACAGTGAAGCTCTTTCATCTGTGAGCTGGTATGCGCCCTGGACTACGCAACAG 468

QY 421 CGCATCAATTCACAGGATATGAAGCCTGACAAATATTTTACTTGAAGAAATCGGCACGTG 480
 DB 469 CGCATCAATTCACAGGATATGAAGCCTGACAAATATTTTACTTGAAGAAATCGGCACGTG 528
 QY 481 CACATCACAGATTTCAACATTCGTGGATGCTGCCAGGGAGACACAGATTAACCACTG 540
 DB 529 CACATCACAGATTTCAACATTCGTGGATGCTGCCAGGGAGATACAGATTAACCACTG 588
 QY 541 GCTGGCACCAGCCTTACATGCACTGAGATGTTTCAGCTCCAGAAAAGGAGCAGGCTAT 600
 DB 589 GCTGGCACCAGCCTTACATGCACTGAGATGTTTCAGCTCCAGAAAAGGAGCAGGCTAT 648
 QY 601 TCTTTGCTGTTGACTGGTGGTCCCTGGGAGTGACGCATATGAACCTCTGAGAGCGCG 660
 DB 649 TCTTTGCTGTTGACTGGTGGTCCCTGGGAGTGACGCATATGAACCTCTGAGAGCGCG 708
 QY 661 AGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATGTATACACAGCTTTCAGAGC 720
 DB 709 AGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATGTATACACAGCTTTCAGAGC 768
 QY 721 ACTGTTGTAACCTTACCTTCTGCTGCTCAGAGGAATGGTCTCACTTCTTAAAAGCTA 780
 DB 769 ACTGTTGTAACCTTACCTTCTGCTGCTCAGAGGAATGGTCTCACTTCTTAAAAGCTA 828
 QY 781 CTCGAACCTTAATCCAGACCAACGATTTTCTCAGTTATCTGATGTCCAGAACTTCCCGTAT 840
 DB 829 CTCGAACCTTAATCCAGACCAACGATTTTCTCAGTTATCTGATGTCCAGAACTTCCCGTAT 888
 QY 841 ATGAATGATATAAATCGGATGCTGCTTTTTCAGAGAGGCTCATTCAGGTTTTCATTCCT 900
 DB 889 ATGAATGATATAAATCGGATGCTGCTTTTTCAGAGAGGCTCATTCAGGTTTTCATTCCT 948
 QY 901 AATAAGGAGGCTGAAATGTGATCCTACCTTTGAACTTGAGGAATGATTTTGAGTCC 960
 DB 949 AATAAGGAGGCTGAAATGTGATCCTACCTTTGAACTTGAGGAATGATTTTGAGTCC 1008
 QY 961 AAACCTCTACATAAGAAAAAAGGCTCTGGCAAGAGAGGAGATATCAGGAATGC 1020
 DB 1009 AAACCTCTACATAAGAAAAAAGGCTCTGGCAAGAGAGGAGATATCAGGAATGC 1068
 QY 1021 GATTCCTCTCAGACATGCTCTTCAAGACACCTTGATCTGTCCAGAGAGGATTCATA 1080
 DB 1069 GATTCCTCTCAGACATGCTCTTCAAGAGCACCCTTGATCTGTCCAGAGAGGATTCATA 1128
 QY 1081 ATTTTCAACAGAAAAAGTAAACAGGACTTTTAAACAAAGACACCAAACTTAGCCTTG 1140
 DB 1129 ATTTTCAACAGAAAAAGTAAACAGGACTTTTAAACAAAGACACCAAACTTAGCCTTG 1188
 QY 1141 GAAACCAACAGACCCCAAGTGACAAATGGACAAATGGACA 1183
 DB 1189 GAAACCAACAGACCCCAAGGTGAGGATGTCAGATAACA 1231

RESULT 9

ACA62840.
 ID ACA62840 standard; cDNA; 1485 BP.

XX AC ACA62840;

DT 01-SEP-2003 (first entry)

XX cDNA encoding human kinase.

KW Human; ss; gene; kinase; gene therapy; cancer; inflammation; psoriasis;
 KW arteriosclerosis.

OS Homo sapiens.

Key Location/Qualifiers

5'UTR 1..2

FT /*tag= a

FT 3..1193

FT /*tag= b

FT 3'UTR /product= "Kinase"
 FT 1194..1475
 XX /*tag= C

FN US2003027307-A1.

XX 06-FEB-2003.

XX 26-SEP-2002; 2002US-00254869.

XX 09-MAR-2001; 2001US-00801876.

XX (APPL-) APPLERA CORP.

XX Ye J, Yan C, Di Francesco V, Beasley EM;

XX WPI; 2003-492035/58.

XX P-PSDB; ABU62276.

PT New isolated human kinase proteins, useful for treating disorders
 PT mediated by kinase pathway (e.g. cancers, inflammations, arteriosclerosis
 PT or psoriasis), or for development of human therapeutics and diagnostic
 PT compositions.

XX Claim 4; Fig 1; 185pp; English.

XX The invention relates to a new isolated human kinase peptide. The human
 CC kinase peptide and nucleic acid molecules are useful in the development
 CC of human therapeutics and diagnostic compositions. The peptides are
 CC useful for treating disorders (e.g. cancers, inflammations,
 CC arteriosclerosis or psoriasis) characterised by an absence of,
 CC inappropriate, or unwanted expression of the kinase protein. These
 CC molecules are particularly useful as models for developing human
 CC therapeutic targets, identifying therapeutic proteins, or serving as
 CC targets for the development of human therapeutic agents that modulate
 CC kinase activity in cells and tissues that express the kinase. The
 CC peptides are also useful for raising antibodies or eliciting an immune
 CC response; as a reagent (including the labelled reagent) in assays
 CC designed to quantitatively determine levels of the protein (or its
 CC binding partner or ligand) in biological fluids; or as markers for
 CC tissues in which the corresponding protein is preferentially expressed.
 CC The agents identified are useful for treating a subject with a disorder
 CC mediated by kinase pathway. The present sequence represents cDNA encoding
 CC a human kinase

XX Sequence 1485 BP; 471 A; 316 C; 331 G; 367 T; 0 U; 0 Other;

Query Match 94.8%; Score 1160.6; DB 9; Length 1485;

Best Local Similarity 98.8%; Pred. No. 0;

Matches 1169; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 ATGGAGCCCAACACTTCAAGAAACCAACCAAGTGTGATGAAATGAAGATGCACTTT 60

DB 3 ATGGAGCCCAACACTTCAAGAAACCAACCAAGTGTGATGAAATGAAGATGCACTTT 62

QY 61 GACCCTTTGAAATTTTGGAGCCATTGGGAAAGGAGTGTGGAAGGCTCTGCATTGTA 120

DB 63 GACCCTTTGAAATTTTGGAGCCATTGGGAAAGGAGTGTGGAAGGCTCTGCATTGTA 122

QY 121 CAGAAGAATGATACCAAGAAGATGTAGCAATCAAGTACATGATAAACAAGATGCGTG 180

DB 123 CAGAAGAATGATACCAAGAAGATGTAGCAATCAAGTACATGATAAACAAGATGCGTG 182

QY 181 GAGCGCAATGAAGTGAGAAATGCTTCAAGGAATCTCAGATCATGAGGGTCTGGAGCAC 240

DB 183 GAGCGCAATGAAGTGAGAAATGCTTCAAGGAATCTCAGATCATGAGGGTCTGGAGCAC 242

QY 241 CTTTCTCTGGTTAATTTGTGGTATCTCTCAAGATGAGGAACATGTTTCATGGTGGTG 300

DB 243 CTTTCTCTGGTTAATTTGTGGTATCTCTCAAGATGAGGAACATGTTTCATGGTGGTG 302

QY 301 GACCTCTCTGGTGGAGACCTGCGTTATCCTCGAACAGAACGTCACCTTCAAGGAA 360

Db 303 GACCTCTGCTGGGTGGAGACCTGGTTATCACCTGCAACAGAACGTCCTCAAGGAA 362
Qy 361 GAAACAGTGAAGCTCTTCATCTGTGAGCTGTGTCATGCGCCCTGGACTACTCGCAACAG 420
Db 363 GAAACAGTGAAGCTCTTCATCTGTGAGCTGTGTCATGCGCCCTGGACTACTCGCAACAG 422
Qy 421 CGCATCATTCACAGGGATATGAAGCTTGACAAATATTTTACTTGGACGAACATGGGCAGTG 480
Db 423 CGCATCATTCACAGGGATATGAAGCTTGACAAATATTTTACTTGGACGAACATGGGCAGTG 482
Qy 481 CACATCAGAGATTTCAACATTTGCGATGTCGATGTCGCCAGGAGACACAGATTTACCACCATG 540
Db 483 CACATCAGAGATTTCAACATTTGCGATGTCGATGTCGCCAGGAGACACAGATTTACCACCATG 542
Qy 541 GCTGGCCACCAAGCCTTACATGGGACCTGAGATGTTTCAGCTCCAGAAAGGAGCAGGCTAT 600
Db 543 GCTGGCCACCAAGCCTTACATGGGACCTGAGATGTTTCAGCTCCAGAAAGGAGCAGGCTAT 602
Qy 601 TCCTTTGCTGTGACTGGTGTGCTGGAGTGACGGATATGAACTGCTGAGAGGCCGG 660
Db 603 TCCTTTGCTGTGACTGGTGTGCTGGAGTGACGGATATGAACTGCTGAGAGGCCGG 662
Qy 661 AGACCGTATCATATTCGCTCCAGTACTTCCAGCAGGAAATTTGACACACGTTTGGAGACG 720
Db 663 AGACCGTATCATATTCGCTCCAGTACTTCCAGCAGGAAATTTGACACACGTTTGGAGACG 722
Qy 721 ACTGTGTAACTTACCTTTCGCTGCTGTCAGAGAAATGTTGTCACCTTTTAAAGGCTA 780
Db 723 ACTGTGTAACTTACCTTTCGCTGCTGTCAGAGAAATGTTGTCACCTTTTAAAGGCTA 782
Qy 781 CTCGAACCTAATCAGACCAACGATTTCTCAGTATCTGATGTCGAGACTTCCGCTAT 840
Db 783 CTCGAACCTAATCAGACCAACGATTTCTCAGTATCTGATGTCGAGACTTCCGCTAT 842
Qy 841 ATGAATGATATAAATCGGATGCGAGTTTTCAGAGAGGCTCATTCAGGTTTCATTCCT 900
Db 843 ATGAATGATATAAATCGGATGCGAGTTTTCAGAGAGGCTCATTCAGGTTTCATTCCT 902
Qy 901 AATAAGGCGGCTGAAATTTGTGATCCTACCTTTGAACCTTTGAGGAAATGATTTGGAGTCC 960
Db 903 AATAAGGCGGCTGAAATTTGTGATCCTACCTTTGAACCTTTGAGGAAATGATTTGGAGTCC 962
Qy 961 AAACCTCTACATAGAAAAAAGGCTGCGCAAGAGGAGAGGATATGAGGAATGC 1020
Db 963 AAACCTCTACATAGAAAAAAGGCTGCGCAAGAGGAGAGGATATGAGGAATGC 1022
Qy 1021 GATTCCTCTCAGACATGCTTCTTCAAGACACCTTGTACTCTGTCCAGAGGAGTTTCA 1080
Db 1023 GATTCCTCTCAGACATGCTTCTTCAAGACACCTTGTACTCTGTCCAGAGGAGTTTCA 1082
Qy 1081 ATTTTCAACAGAGAAAAAGTAAACAGGACCTTTTAAACAAAGCAACCAATCTAGCCTTG 1140
Db 1083 ATTTTCAACAGAGAAAAAGTAAACAGGACCTTTTAAACAAAGCAACCAATCTAGCCTTG 1142
Qy 1141 GAACAAACCAAGACCCCAAGTGCACAAATGGACAAATGGACA 1183
Db 1143 GAACAAACCAAGACCCCAAGAGTGGAGATGGTCAGATAACA 1185

RESULT 10

AB55499 ID AB55499 standard; cDNA; 1485 BP.

XX AC

XX AC

XX AC

XX 14-JAN-2003 (first entry)

XX cDNA encoding human serine/threonine protein kinase-like kinase.

XX Human; kinase; serine/threonine kinase; immune response; transgenic;
XX gene therapy; chromosome 5; gene; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

PH 5'UTR 1..2

FT /*tag= a

FT CDS 3..1193

FT /*tag= b

FT 3'UTR /product= "Serine/threonine protein kinase-like kinase"

FT 1194..1485

FT /*tag= c

XX US2002127683-A1.

XX PN 12-SEP-2002.

XX 09-MAR-2001; 2001US-00801876.

XX 09-MAR-2001; 2001US-00801876.

XX (YELJ/) YE J.

XX (YANC/) YAN C.

XX (DFRA/) DI FRANCESCO V.

XX (BEAS/) BEASLEY E M.

XX Ye J, Yan C, Di Francesco V, Beasley EM;

XX WPI; 2003-028938/02.

XX P-PSDB; ABG70700.

XX Novel isolated human kinase peptide useful for treating disorder
XX characterized by absence of, in appropriate or unwanted expression of the
XX kinase protein, and as immunogens to raise antibodies.

XX Claim 4; Fig 1; 174pp; English.

XX The present invention relates to the isolation of a human kinase and the
XX polynucleotide sequences encoding it. The human kinase of the invention
XX is related to the serine/threonine kinase subfamily. The gene encoding
XX the human kinase is located on chromosome 5. The polypeptide and
XX polynucleotide sequences of the invention are useful for treating a
XX disease or condition mediated by a human kinase. Both the polypeptide and
XX polynucleotide sequences are useful as models for the development of
XX human therapeutics, for identifying therapeutic proteins, as targets for
XX development of human therapeutic agents, and as query sequences to
XX perform a search against sequence data bases to identify other family
XX members of related sequences. The polypeptide is useful to raise
XX antibodies or to elicit another immune response, as a reagent in assays
XX designed to quantitatively determine levels of the protein in biological
XX fluids, as markers for tissues in which the corresponding protein is
XX preferentially expressed, in drug screening assays, in cell-based or cell
XX -free systems, to identify compounds that modulate kinase activity of the
XX protein in its natural state, or an altered form that causes the specific
XX disease or pathology associated with the kinase, to screen a compound for
XX the ability to stimulate or inhibit interaction between the kinase
XX protein and a molecule that normally interacts with the kinase protein,
XX and in pharmacogenomic analysis. The polynucleotide is useful for
XX monitoring the effectiveness of modulating compounds on the expression or
XX activity of the human kinase gene in clinical trials or in a treatment
XX regimen, in diagnostic assays for qualitative changes in a human kinase
XX nucleic acid that leads to a pathology, for testing an individual for a
XX genotype that while not necessarily causing a disease, nevertheless
XX affects the treatment modality, as antisense constructs to control human
XX kinase gene expression in cells, tissues and organisms, for gene therapy
XX in patients containing cells that are aberrant in human kinase gene
XX expression, and to produce transgenic animals. The present sequence
XX encodes a human kinase related to the serine/threonine protein kinase
XX subfamily

XX Sequence 1485 BP; 471 A; 316 C; 331 G; 367 T; 0 U; 0 Other;

Query Match 94.8%; Score 1160.6; DB 10; Length 1485;

Best Local Similarity 98.8%; Pred. No. 0;

Matches 1169; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

```
QY 1 ATGGAGCCCAACACCTTCAAGAAACCAACAGTGTGTTGATGAAAAATCAAGATGCAACTTT 60
Db 1 ATGGAGCCCAACACCTTCAAGAAACCAACAGTGTGTTGATGAAAAATCAAGATGCAACTTT 62
QY 61 GACCACTTTGAAATTTTGGAGCCATTTGGAAAGGCGATTTTGGAGAGTCTGCAATTGTA 120
Db 63 GACCACTTTGAAATTTTGGAGCCATTTGGAAAGGCGATTTTGGAGAGTCTGCAATTGTA 122
QY 121 CAGAAGATGATACCAAGAGATGTACGCAATGAGTACATGAATAAACAAGAGTGGTG 180
Db 123 CAGAAGATGATACCAAGAGATGTGCGCAATGAGTACATGAATAAACAAGAGTGGTG 182
QY 181 GAGCGCAATGAGTGAAGATGTCTTCAAGAACTCCAGATCATCGAGGCTCTGGAGCAC 240
Db 183 GAGCGCAATGAGTGAAGATGTCTTCAAGAACTCCAGATCATCGAGGCTCTGGAGCAC 242
QY 241 CTTTTCCTGGTTAAATTTGGTGTATTCCTCCAGATGAGGAAGACATGTTTCATGTTGTG 300
Db 243 CTTTTCCTGGTTAAATTTGGTGTATTCCTCCAGATGAGGAAGACATGTTTCATGTTGTG 302
QY 301 GACCTCCTGCTGGTGGAGACCTGCGTTATCACTGCAACAGAACTCCACTTCAAGGAA 360
Db 303 GACCTCCTGCTGGTGGAGACCTGCGTTATCACTGCAACAGAACTCCACTTCAAGGAA 362
QY 361 GAAACAGTGAAGCTCTTCACTGTGAGTGTGTCATGGCCCTGGAATCACTGCAGAACCA 420
Db 363 GAAACAGTGAAGCTCTTCACTGTGAGTGTGTCATGGCCCTGGAATCACTGCAGAACCA 422
QY 421 CCGCATCATTCACAGGATATGAAGCTGACATATTTTACTTGAGCAACATGGGCACTG 480
Db 423 CCGCATCATTCACAGGATATGAAGCTGACATATTTTACTTGAGCAACATGGGCACTG 482
QY 481 CACATCACAGATTTCAACATTTCTGCGATGCTGCCAGGAGACACAGATTACCAACATG 540
Db 483 CACATCACAGATTTCAACATTTCTGCGATGCTGCCAGGAGACACAGATTACCAACATG 542
QY 541 GCTGCGACCAAGCTTACATGCACTGAGATGTTTCACTCAGAAAAGGAGCGAGGTAT 600
Db 543 GCTGCGACCAAGCTTACATGCACTGAGATGTTTCACTCAGAAAAGGAGCGAGGTAT 602
QY 601 TCCCTTGTGTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
Db 603 TCCCTTGTGTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 662
QY 661 AGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTTGACACAGCTTTGAGACG 720
Db 663 AGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTTGACACAGCTTTGAGACG 722
QY 721 ACTGTTGTAACTTACCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Db 723 ACTGTTGTAACTTACCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 782
QY 781 CTGGAACCTAATCCAGACCAACGATTTTCTCAGTTATCTGATGTCAGAACTTCCCGTAT 840
Db 783 CTGGAACCTAATCCAGACCAACGATTTTCTCAGTTATCTGATGTCAGAACTTCCCGTAT 842
QY 841 ATGAATGATATAAATCGGATGCACTTTTTCAGAAAGGCTCATTTCCAGGTTTCATTCCT 900
Db 843 ATGAATGATATAAATCGGATGCACTTTTTCAGAAAGGCTCATTTCCAGGTTTCATTCCT 902
QY 901 AATAAGGAGCGCTGAATTTGTGATCCTACCTTTCAGAACTTTCAGAACTTTCAGGATCC 960
Db 903 AATAAGGAGCGCTGAATTTGTGATCCTACCTTTCAGAACTTTCAGAACTTTCAGGATCC 962
QY 961 AAACCTCTACATAAGAAAAAAGCGTCTGGCAAGAGGAGAGGATATCAGGAATGTC 1020
Db 963 AAACCTCTACATAAGAAAAAAGCGTCTGGCAAGAGGAGAGGATATCAGGAATGTC 1022
QY 1021 GATTCCTTCTCAGACATGCTTCTTCAAGAGCACCTTGTGCTGTGTCAGAGAGGATTCATA 1080
Db 1023 GATTCCTTCTCAGACATGCTTCTTCTTCAAGAGCACCTTGTGCTGTGTCAGAGAGGATTCATA 1082
QY 1081 ATTTTCAACAGAGAAAAAGTAAACAGGAGCTTTTAAACAAAGACCAACCAATCTAGCCTTG 1140
```

```
Db 1083 ATTTTCAACAGAGAAAAAGTAAACAGGAGCTTTTAAACAAAGACCAACCAATCTAGCCTTG 1142
QY 1141 GAACAAACCAAGACCCCAAGTGCACAAATGGACAAATGGACA 1183
Db 1143 GAACAAACCAAGACCCCAAGTGCACAAATGGTGCAGATATACA 1185

RESULT 11
ADL09161
ID ADL09161 standard; cDNA; 1485 BP.
XX AC ADL09161;
XX DT 20-MAY-2004 (first entry)
XX DE Human protein kinase, cDNA.
XX KW gene; ss; human; Kinase Modulator;
XX KW serine/threonine protein kinase subfamily; Gene Therapy; protein kinase.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX CDS 3..1193
XX FT /*tag= a
XX FT /product= "Human protein kinase"
XX PN US2004043466-A1.
XX PD 04-MAR-2004.
XX PF 23-SEP-2003; 2003US-00667442.
XX PR 09-MAR-2001; 2001US-00801876.
XX PR 26-SEP-2002; 2002US-00254869.
XX PA (APPL-) APPLERA CORP.
XX PI Ye J, Yan C, Di Francesco V, Beasley EM;
XX WPI; 2004-280746/26.
XX DR P-PSDB; ADL09162.
XX
XX New isolated human kinase peptides, useful as models for developing human
XX therapeutic targets, aid in the identification of therapeutic proteins,
XX or for diagnosing, preventing and treating kinase-related conditions.
XX
XX Claim 4; SEQ ID NO 1; 184pp; English.
XX
XX The invention relates to new isolated human protein kinase polypeptide
XX and polynucleotides. The new human kinase protein is related to the
XX serine/threonine protein kinase subfamily. The kinase peptides and
XX nucleic acid molecules are useful as models for the development of human
XX therapeutic targets, aid in the identification of therapeutic proteins,
XX and serve as targets for the development of human therapeutic agents that
XX modulate kinase activity in cells and tissues that express the kinase.
XX The peptides are also useful in the diagnosis, prevention and treatment
XX of kinase-related conditions. The peptide may be used in drug screening,
XX assays, in assays to determine the biological activity of the protein, to
XX raise antibodies or to elicit another immune response, as a reagent in
XX assays designed to quantitatively determine levels of the protein in
XX biological fluids, or as markers for tissues in which the corresponding
XX protein is preferentially expressed. The antibodies are useful in
XX pharmacogenomic analysis, for inhibiting protein function, or for tissue
XX typing. The nucleic acid molecules are useful as probes, primers,
XX chemical intermediates, or in biological assays. The present sequence
XX represents the cDNA encoding the human protein kinase.
XX
XX Sequence 1485 BP; 471 A; 316 C; 331 G; 367 T; 0 U; 0 Other;
XX
XX Query Match 94.8%; Score 1160.6; DB 12; Length 1485;
XX Best Local Similarity 98.8%; Pred. No. 0;
```

Matches 1169; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

```
Qy 1 ATGGGAGCCACACTTCAAGAAAACCCACGCTGTTGATGAAATGAAGATGTCAACTTT 60
Db 3 ATGGGAGCCACACTTCAAGAAAACCCACGCTGTTGATGAAATGAAGATGTCAACTTT 62
Qy 61 GACCACCTTTGAAATTTTCGAGCCATTGGGAAAGCGAGTTTGGGAAAGTCTGCATTGTA 120
Db 63 GACCACCTTTGAAATTTTCGAGCCATTGGGAAAGCGAGTTTGGGAAAGTCTGCATTGTA 122
Qy 121 CAGAAGATGATACCAAGAGATGTACGCAATGAAGTACATGAATAAACAAGTGGGTG 180
Db 123 CAGAAGATGATACCAAGAGATGTGCGCAATGAAGTACATGAATAAACAAGTGGGTG 182
Qy 181 GAGCGCAATGAGTGAAGAAATGCTTCAAGAACTCCAGATCATCGAGGTCTGGAGCAC 240
Db 183 GAGCGCAATGAGTGAAGAAATGCTTCAAGAACTCCAGATCATCGAGGTCTGGAGCAC 242
Qy 241 CCTTTCCTGGTTAATTTGTGGTATTTCTTCCAAGATGAGGAAGACATGTTTCATGTTGTG 300
Db 243 CCTTTCCTGGTTAATTTGTGGTATTTCTTCCAAGATGAGGAAGACATGTTTCATGTTGTG 302
Qy 301 GACCTCTCTGCTGGTGGAGACTCGCTTATCACTGCAACAGAACGTCCTCAAGGAA 360
Db 303 GACCTCTCTGCTGGTGGAGACTCGCTTATCACTGCAACAGAACGTCCTCAAGGAA 362
Qy 361 GAAACAGTGAAGCTTCACTGTGAGCTGTGTCATGCGCCCTGGACTACCTCGAGAACG 420
Db 363 GAAACAGTGAAGCTTCACTGTGAGCTGTGTCATGCGCCCTGGACTACCTCGAGAACG 422
Qy 421 CGCATCATTCACAGGAGATGAAGCCTGACAAATATTTTACTTGACGAACATGGCGACGTG 480
Db 423 CGCATCATTCACAGGAGATGAAGCCTGACAAATATTTTACTTGACGAACATGGCGACGTG 482
Qy 481 CACATCAGATTTCAACATTTGCTGCGATGCTGCCAGGAGACACAGATTTACCACCATG 540
Db 483 CACATCAGATTTCAACATTTGCTGCGATGCTGCCAGGAGACACAGATTTACCACCATG 542
Qy 541 GCTGGCCACCAAGCCTTACATGGCACTGAGATGTTCAAGTCCAGAAAAGGAGCGAGTAT 600
Db 543 GCTGGCCACCAAGCCTTACATGGCACTGAGATGTTCAAGTCCAGAAAAGGAGCGAGTAT 602
Qy 601 TCCCTTCTGTTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
Db 603 TCCCTTCTGTTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 662
Qy 661 AGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTTGACACACGTTTGAGACG 720
Db 663 AGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTTGACACACGTTTGAGACG 722
Qy 721 ACTGTTGTAACCTTACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
Db 723 ACTGTTGTAACCTTACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 782
Qy 781 CTGCAACTAATCAGACCAACGATTTCTCAGTATCTGATGTCAGAACTTCCCGTAT 840
Db 783 CTGCAACTAATCAGACCAACGATTTCTCAGTATCTGATGTCAGAACTTCCCGTAT 842
Qy 841 ATGAATGATATAAAGTGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
Db 843 ATGAATGATATAAAGTGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 902
Qy 901 AATAAGGCGAGGCTGAATTTGATGCTTCACTTCTGAGTGTGAGGAATGATTTTGGAGTCC 960
Db 903 AATAAGGCGAGGCTGAATTTGATGCTTCACTTCTGAGTGTGAGGAATGATTTTGGAGTCC 962
Qy 961 AAACCTCTACATAGAAAAAAGCGCTGCGAAAGAGGAGGATATGAGGAATGC 1020
Db 963 AAACCTCTACATAGAAAAAAGCGCTGCGAAAGAGGAGGATATGAGGAATGC 1022
Qy 1021 GATTCCTCTCAGACATGCTTCTTCAAGAGCACCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
Db 1023 GATTCCTCTCAGACATGCTTCTTCAAGAGCACCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 1082
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```
Qy 1081 ATTTTCAACAGAGAAAAAGTAAACAGGACTTTTAAACAAAACACAAATCTAGCCTTG 1140
Db 1083 ATTTTCAACAGAGAAAAAGTAAACAGGACTTTTAAACAAAACACAAATCTAGCCTTG 1142
Qy 1141 GAACAAACCAAAAGACCCACCAAGTGACAAATGGACAAATGGACA 1183
Db 1143 GAACAAACCAAAAGACCCACCAAGGTGAGGNTGGTCAGATAACA 1185
```

RESULT 12

ADM01546

ID ADM01546 standard; cDNA; 2063 BP.

XX ADM01546;

XX 20-MAY-2004 (first entry)

XX Human cDNA of the invention SEQ ID NO:231.

XX ss; gene; human; gene therapy; diagnostic marker; pharmaceutical.

XX Homo sapiens.

XX EPI347046-A1.

XX 24-SEP-2003.

XX 12-APR-2002; 2002EP-00008400.

XX 22-MAR-2002; 2002JP-00137785.

XX (REAS-) RES ASSOC BIOTECHNOLOGY.

PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;

XX WPI; 2003-723558/69.

XX P-PSDB; ADM03989.

XX New polynucleotides and polypeptides are useful in gene therapy, for
developing a diagnostic marker or medicines for regulating their
expression and activity, or as a target of gene therapy.

XX Claim 1; SEQ ID NO 231; 305pp; English.

XX The invention relates to a novel human polynucleotide and the encoded
polypeptide. A polynucleotide of the invention may have a use in gene
therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful
as a primer for synthesizing the polynucleotide or as a probe for
detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are
useful in gene therapy, for developing a diagnostic marker or medicines
for regulating their expression and activity, or as a target of gene
therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides
are useful as pharmaceutical agents. The present sequence represents a
cDNA sequence of the invention.

XX Sequence 2063 BP; 556 A; 463 C; 500 G; 544 T; 0 U; 0 Other;

Query Match 84.3%; Score 1032.2; DB 11; Length 2063;

Best Local Similarity 99.7%; Pred. No. 4e-290;

Matches 1034; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATGGGAGCCCAACACTTCAAGAAAACCCACCAAGTGTTCATGATAAATGAAGATGTCAACTTT 60

Db 334 ATGGGAGCCCAACACTTCAAGAAAACCCACCAAGTGTTCATGATAAATGAAGATGTCAACTTT 393

Qy 61 GACCACCTTTGAAATTTTTCGAGCCATTGGGAAAGCGAGTTTGGGAAAGGCTCTGCATTGTA 120

Db 394 GACCACCTTTGAAATTTTTCGAGCCATTGGGAAAGCGAGTTTGGGAAAGGCTCTGCATTGTA 453

Qy 121 CAGAAAGATGATACCAAGAGATGTACGCAATGAAGTACATGAATAAACAAGTGGGTG 180

Db 1332 ATTTTCAACAGAGAAAAGTAAAGTGACTTTAATCAGACAGCAAGCAAAATCTAGCCTTG 1391

QY 1141 GAACAAACCAAGAC 1155

Db 1392 GAACAAACCAAAAC 1406

RESULT 14

ADF44497

ID ADF44497 standard; cDNA; 3766 BP.

XX

AC ADF44497;

XX

DT 12-FEB-2004 (first entry)

XX

DE Mouse kinase protein encoding cDNA SEQ ID NO:15.

XX

KW cytostatic; neutropic; neuroprotective; antidiabetic; screening;

KW regulation; drug development; protein-associated disease; cancer;

KW dementia; diabetes; kinase; enzyme; mouse; gene; ss.

XX

OS Mus musculus.

XX

PN W0203084992-A1.

XX

PD 16-OCT-2003.

XX

PF 04-APR-2003; 2003WO-JP004330.

XX

PR 05-APR-2002; 2002JP-00103396.

PR 23-APR-2002; 2002JP-00120904.

PR 04-MAY-2002; 2002JP-00130601.

PR 04-DEC-2002; 2002JP-00352520.

XX

XX (RIKE) RIKEN KK.

PA (DNAF-) DNAFORM KK.

XX

PA (MITU) MITSUBISHI CHEM CORP.

XX

PI Hayaehizaki Y, Kamiya M, Kubodera H, Watanabe W;

DR WPI; 2003-833568/77.

DR P-PSDB; ADF44523.

XX

PT Proteins and encoded DNAs with kinase activity, useful in screening

PT substances for regulating such activity and in developing drugs for the

PT protein-associated diseases e.g. cancer, dementia and diabetes.

XX

PS Claim 4; SEQ ID NO 15; 342pp; Japanese.

XX

CC The present invention describes a protein: (a) containing any of the

CC amino acid sequences of ADF44509 to ADF44534 or ADF44544; or (b) based on

CC any of the sequences in (a) but with some amino acids deleted.

CC substituted and/or added and having kinase activity. Also described: (1)

CC a DNA encoding any of the proteins; (2) a full-length cDNA encoding the

CC protein; (3) a DNA which is: (a) a DNA containing any of the base

CC sequences in ADF44483 to ADF44508 or ADF44543; (b) a DNA derived from any

CC of the sequences in (a) but with some bases deleted, substituted and/or

CC added and encoding a protein with kinase activity; or (c) a DNA

CC hybridisable with any of the sequences in (a) or their complementary

CC strands under stringent conditions and encoding a protein with kinase

CC activity; (4) a recombinant vector containing the DNA; (5) a cell

CC transfected with the DNA or recombinant vector, or an individual produced

CC from the cell; (6) recombinant proteins produced by such cells; (7) an

CC oligonucleotide containing 5-10 consecutive bases in any of the base

CC sequences, its sense oligonucleotide, an antisense oligonucleotide with a

CC complementary strand of such sense oligonucleotide, or an oligonucleotide

CC derivative of the (anti)-sense oligonucleotide; (8) an antibody

CC specifically binding to the protein, or its partial fragment; (9) a

CC method for screening substances for regulating activity of the protein by

CC contacting a test substance with such protein before measuring changes in

CC the protein activity due to the test substance; (10) a method for

CC screening substances regulating expression of the DNA by contacting a

CC disorders (e.g. schizophrenia), neurodegenerative disorders (e.g.
CC Parkinson's disease), inflammatory disorders (e.g. asthma), infectious
CC disease (e.g. HIV) and reproductive disorders (e.g. infertility).
CC Additionally, polynucleotides encoding protein kinases may be used for
CC gene therapy and as DNA probes in diagnostic assays. The protein kinase
CC polypeptides may be used as antigens in the production of antibodies
CC against the protein kinases and in assays to identify modulators of
CC protein kinase expression and activity
XX
SQ Sequence 981 BP; 294 A; 207 C; 245 G; 235 T; 0 U; 0 Other;

Query Match 68.0%; Score 832.8; DB 4; Length 981;
Best Local Similarity 90.8%; Pred. No. 4.3e-232;
Matches 904; Conservative 0; Mismatches 77; Indels 15; Gaps 1;

Qy 1 ATGGGAGCCACACTTCAAGAAAAACCACAGTGTGATGAAATGAAGATGTCAACTTT 60
Db 1 ATGGGAGCCACACTTCAAGAAAAACCACAGTGTGATGAAATGAAGATGTCAACTTT 60

Qy 61 GACCACTTGAATTTTGGAGCCATTGGGAAGGCAGTTTGGGAAGGCTCGCATTTGA 120
Db 61 GACCACTTGAATTTTGGAGCCATTGGGAAGGCAGTTTGGGAAGGCTCGCATTTGA 120

Qy 121 CAGAAGATGATACCAAGAGATGTAGCAATGAAGTACATGAATAAACAAGTGGGTG 180
Db 121 CAGAAGATGATACCAAGAGATGTAGCAATGAAGTACATGAATAAACAAGTGGGTG 180

Qy 181 GAGCGCAATGAAGTGAAGAAATGTCTTCAAGAACTCCAGATCATCGAGGGTCTCGAGCAC 240
Db 181 GAGCGCAATGAAGTGAAGAAATGTCTTCAAGAACTCCAGATCATCGAGGGTCTCGAGCAC 240

Qy 241 CTTTTCTGGTTAATTTGTGGTATTTCTTCAAGATGAGGAGACATGTTTCATGGTGGTG 300
Db 241 CTTTTCTGGTTAATTTGTGGTATTTCTTCAAGATGAGGAGACATGTTTCATGGTGGTG 300

Qy 301 GACCTCTGCTGGGTGGAGACTCGGTTATCACCTGCAACAGAACCTCCACTTCAAGGAA 360
Db 301 GACCTCTGCTGGGTGGAGACTCGGTTATCACCTGCAACAGAACCTCCACTTCAAGGAA 360

Qy 361 GAAACAGTGAAGCTCTTCACTGTGAGCTGGTCAATGTCCTGGAGTACCTGCGAACCCAG 420
Db 361 GAAACAGTGAAGCTCTTCACTGTGAGCTGGTCAATGTCCTGGAGTACCTGCGAACCCAG 420

Qy 421 CGCATCATTCACAGGATATGAAGCTGACATATTTTACTTTGACGACATGCGGCACGTG 480
Db 421 CGCATCATTCACAGGATATGAAGCTGACATATTTTACTTTGACGACATGCGGCACGTG 480

Qy 481 CACATCAGATTTTCAACATTTGCTGCGATGCTGCCAGGAGACACAGATTACCACCATG 540
Db 481 CACATCAGATTTTCAACATTTGCTGCGATGCTGCCAGGAGACACAGATTACCACCATG 540

Qy 541 GCTGGCACCAAGCCTTACATGGCACCTGAGATGTTTCAAGTCCAGAAAAAGGAGCGGTAT 600
Db 541 GCTGGCACCAAGCCTTACATGGCACCTGAGATGTTTCAAGTCCAGAAAAAGGAGCGGTAT 600

Qy 601 TCCTTTGCTGTGATGCTGCTGCTGGAGTACGCGATATGAATCTGCTGAGAGGCGGG 660
Db 601 TCCTTTGCTGTGATGCTGCTGCTGGAGTACGCGATATGAATCTGCTGAGAGGCGGG 660

Qy 661 AGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTTGACACAGCTTTGAGACG 720
Db 661 AGACCGTATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTTGACACAGCTTTGAGACG 720

Qy 721 ACTGTTGTAACTTACCTTCTGCTGGTCAAGGAAATGTTGTCACCTTTTAAAGGCTA 780
Db 721 ACTGTTGTAACTTACCTTCTGCTGGTCAAGGAAATGTTGTCACCTTTTAAAGGCTA 780

Qy 781 CTCGAACTTAATCAGACCAACAGATTTTCTCAGTTATCTGATGTCAGAACTTCCCGTAT 840
Db 781 AGAAGGAAGACTGCATGTC-----CAACGGAAGTAACAAAAGGAAGCAGG 825

Qy 841 ATGAATGATATAAAGTGGATGTCAGTTTTCAGAGAGGCTCATTCAGAGTTTCATTCCT 900

Db 826 CTCCTCGCTTAAGTTTAGAAGTTTAGTATACAAATATTGGGACACCAACTGCTTCTCTTG 885
Qy 901 AATRAAGGCGAGGCTGAATTTGTGATCCTACCTTTGAACCTTGAGGAATGATTTTGGAGTCC 960
Db 886 CAGAAAGGCGAGGCTGAATTTGTGATCCTACCTTTGAACCTTGAGGAATGATTTTGGAGTCC 945
Qy 961 AAACCTCTACATAAGAAAAAAGCGTCTGGCAAG 996
Db 946 AAACCTCTACATAAGAAAAAAGCGTCTGGCAAG 981

Search completed: December 20, 2004, 04:50:36
Job time : 473 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 20, 2004, 02:05:31 ; Search time 3705 Seconds
(without alignments)
15622.832 Million cell updates/sec

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Perfect score: 1224
Sequence: 1 atgggagccacacttcaag.....agacctgaaagtctcataa 1224

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_hcg.*
- 3: gb_in.*
- 4: gb_on.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pi.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1224	100.0	1224	6	AR393902 Sequence
2	1224	100.0	1224	6	AX303183 Sequence
3	1224	100.0	1675	6	AR393904 Sequence
4	1224	100.0	1675	6	AX303187 Sequence
5	1165.4	95.2	1191	6	AR393903 Sequence
6	1165.4	95.2	1191	6	AX303185 Sequence
7	1165.4	95.2	1594	6	AX207388 Sequence
8	1165.4	95.2	1594	6	AX766348 Sequence
9	1163.8	95.1	1191	6	AX320936 Sequence
10	1163.8	95.1	1281	6	AX320934 Sequence
11	1160.6	94.8	1485	6	AR265353 Sequence
12	1160.6	94.8	1485	6	AR432044 Sequence
13	1032.2	84.3	2063	6	AX833107 Sequence
14	1032.2	84.3	2063	9	AK094580 Homo sapi
15	832.8	68.0	981	6	AX166513 Sequence
16	773	63.2	4973	10	BC055002 Mus muscu
17	726.4	59.3	2229	5	BX950341 Gallus ga
18	661	54.0	711	6	AR393901 Sequence
19	661	54.0	711	6	AX303181 Sequence

20	660	53.9	678	6	AR393900	AR393900 Sequence
21	660	53.9	678	6	AX303179	AX303179 Sequence
22	628.2	51.3	1456	5	BC072876	BC072876 Xenopus l
23	558.4	45.6	3367	10	BC052404	BC052404 Mus muscu
24	558.4	45.6	3367	10	BC058412	BC058412 Mus muscu
25	558.4	45.6	3449	10	BC056396	BC056396 Mus muscu
26	555.2	45.4	2045	10	MMU250840	AJ250840 Mus muscu
27	542.4	44.3	3224	6	AX056360	AX056360 Sequence
28	542.4	44.3	3224	9	HS250839	AX250839 Homo sapi
29	540.8	44.2	3236	9	BC038238	BC038238 Homo sapi
30	519.6	42.5	3244	6	AX376504	AX376504 Sequence
31	519.6	42.5	3244	9	AY358353	AY358353 Homo sapi
32	497.6	40.7	2184	10	BC026457	BC026457 Mus muscu
33	497.6	40.7	2201	10	AB041542	AB041542 Mus muscu
34	484.8	39.6	1257	6	AR411704	AR411704 Sequence
35	484.8	39.6	1826	6	AR411703	AR411703 Sequence
36	484.8	39.6	2143	9	AY098866	AY098866 Homo sapi
37	483.2	39.5	1487	6	AX504245	AX504245 Sequence
38	483.2	39.5	1858	9	BC015792	BC015792 Homo sapi
39	479.4	39.2	1787	6	AX056359	AX056359 Sequence
40	476.4	38.9	2029	9	BC069203	BC069203 Homo sapi
41	472.4	38.6	827	9	BC021666	BC021666 Homo sapi
42	471.6	38.5	2028	9	BC045760	BC045760 Homo sapi
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ALIGNMENTS

RESULT 1
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LOCUS AR393902 1224 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 8 from patent US 6617147.
ACCESSION AR393902
VERSION AR393902.1 GI:40121077
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1224)
AUTHORS Hu, Y., Nepomnich, B., Wang, X. and Donoho, G.
TITLE Human kinase proteins and polynucleotides encoding the same
JOURNAL Patent: US 6617147-A 8 09-SEP-2003;
FEATURES Location/Qualifiers
source 1..1224
/organism="unknown"
/mol_type="genomic DNA"

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Db	1	ATGGAGCCCAACTTCAAGAAACCCACAGTGTGTTGATGAAATGAAGATGTCAACTTT	60
Qy	61	GACCACCTTGAATTTTGGAGCCATTTGGGAAAGGAGTTTGGGAGGTCGCAATCTGA	120
Db	61	GACCACCTTGAATTTTGGAGCCATTTGGGAAAGGAGTTTGGGAGGTCGCAATCTGA	120
Qy	121	CAGAAGATGATCAAGAAAGATGTACGCAATGAAGTACATGAATAAACAAGTCGCTG	180
Db	121	CAGAAGATGATCAAGAAAGATGTACGCAATGAAGTACATGAATAAACAAGTCGCTG	180
Qy	181	GAGCGCAATGAAGTGAAGAAATGTCTTCAAGAACTCCAGATCATCGAGGTCGTGAGCAC	240
Db	181	GAGCGCAATGAAGTGAAGAAATGTCTTCAAGAACTCCAGATCATCGAGGTCGTGAGCAC	240
Qy	241	CCTTTCTGTTAATTTGTGGTATCTCTTCAAGATGAGGAGACATGTTTCATGCTGGTG	300


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Db 781 CTGGAACCTAATCCAGACCAACGATTTTCTCAGTTATCTGATGTCCAGAACTTCCCGTAT 840
QY 841 ATGAATGATATAAATCTGGGATGCAAGTTTTCAGAAAGAGGCTCATTCAGGTTTCATTCCT 900
Db 841 ATGAATGATATAAATCTGGGATGCAAGTTTTCAGAAAGAGGCTCATTCAGGTTTCATTCCT 900
QY 901 AATAAAGGAGGCTGAATTTGATTCCTACCTTTGAACTTGAGGAAATGATTTGGAGTCC 960
Db 901 AATAAAGGAGGCTGAATTTGATTCCTACCTTTGAACTTGAGGAAATGATTTGGAGTCC 960
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Db 1201 TTTTCAGACCTCGAAAGTTTCATAA 1224
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RESULT 3
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LOCUS AR393904 1675 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 12 from patent US 6617147.
ACCESSION AR393904
VERSION AR393904.1 GI:40121081
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 1675)
AUTHORS Hu, Y., Nepomnichy, B., Wang, X. and Donoho, G.
TITLE Human kinase proteins and polynucleotides encoding the same
JOURNAL Patent: US 6617147-A 12 09-SEP-2003;
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location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 8.4e-311;
Matches 1224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 413 ATGGGAGCCACACTTCAAGAAAAACCAACCTGTTTGTATGAAATGAAGATGTCAACTTT 472
QY 61 GACCACCTTGAATTTTTCGAGCCATTGGGAAAGGCGAGTTTGGGAAAGGCTGCAATTGTA 120
Db 473 GACCACCTTGAATTTTTCGAGCCATTGGGAAAGGCGAGTTTGGGAAAGGCTGCAATTGTA 532
QY 121 CAGAAAGATGATACCAAGAGATGTACGATGAAGTACATGAATAACAAAAGTGGGTG 180
Db 533 CAGAAAGATGATACCAAGAGATGTACGATGAAGTACATGAATAACAAAAGTGGGTG 592
QY 181 GAGGCGAATGAAGTGAGAAATGTCTTCAAGGAACTCCAGATCATGGGGTCTGGAGCAC 240
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QY 241 CTTTCTCTGGTTAAATTTGTGGTATTCTTCCNAGATGAGGAAGACATGTTTCATGGTGGTG 300
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QY 301 GACTCTCTGCTGGGTGGAGACCTTGCCTGTTATCCTCTGCAACAGAACTGCTCACTTCAAGGAA 360
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QY 481 CACATCACAGATTTCAACATTTGCTGCGATGCTGCCAGGAGGACACAGATTTACCACCATG 540
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Db 953 GCTGGCACCAAGCTTTACATGGCACTGAGATGTTCAAGTCTCCAGAAAGGAGGAGGCTAT 1012
QY 601 TCCTTTGCTGTTGACTGGTGGTCCCTGGGAGTGACGCGCATATGAACTGCTGAGAGGCGG 660
Db 1013 TCCTTTGCTGTTGACTGGTGGTCCCTGGGAGTGACGCGCATATGAACTGCTGAGAGGCGG 1072
QY 661 AGACCGTATCATATTTGCTCCAGTACTTCCAGCAAGGAAATTTGACACAGCTTTGAGACG 720
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RESULT 4
AX303187
LOCUS

AX303187 1675 bp DNA linear PAT 30-NOV-2001

DEFINITION	Sequence 12 from Patent WO0181557.									
ACCESSION	AX303187									
VERSION	AX303187.1									
KEYWORDS	GI:17383669									
SOURCE	Homo sapiens (human)									
ORGANISM	Homo sapiens									
REFERENCE	Hu, Y., Nepomnichy, B., Wang, X., Donoho, G., Scoville, J. and									
AUTHORS	Walke, D.W.									
TITLE	Human kinase proteins and polynucleotides encoding the same									
JOURNAL	Patent: WO 0181557-A 12 01-NOV-2001;									
FEATURES	Lexicon Genetics Incorporated (US)									
source	Location/Qualifiers									
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	/mol_type="unassigned DNA"									
	/db_xref="taxon:9606"									
ORIGIN										
	Query Match 100.0%; Score 1224; DB 6; Length 1675;									
	Best Local Similarity 100.0%; Pred. No. 8.4e-311;									
	Matches 1224; Conservative 0; Mismatches 0; Indels 0; Gaps 0									
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QY	61	GACCACTTTGAATTTTCGAGGCCATTGGGAAGGCGAGTTTTCGGGAAGCTCTGCATTGTA	120							
Db	473	GACCACTTTGAATTTTCGAGGCCATTGGGAAGGCGAGTTTTCGGGAAGCTCTGCATTGTA	532							
QY	121	CAGAAAGATGATACCAAGAAGATGTACGCAATGAAGTACATGAATATAACAAAGTCGCTG	180							
Db	533	CAGAAAGATGATACCAAGAAGATGTACGCAATGAAGTACATGAATATAACAAAGTCGCTG	592							
QY	181	GAGCCCAATGAGTGAGAAATGTCTTCAAGGAATCCAGATCATGACGGTCTGGAGCAC	240							
Db	593	GAGCCCAATGAGTGAGAAATGTCTTCAAGGAATCCAGATCATGACGGTCTGGAGCAC	652							
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QY	361	GAACAGTGAAGCTCTTCATCTGTGAGCTGGTCAATGGCCCTGGACTTACTCTGAGAACAG	420							
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QY	481	CACATCAGATTTTCAACATTGCTGGATGCTGCCACGGAGACACAGATTACCAACCATG	540							
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QY	661	AGACGGTATCATATTCCTCTCAGTACTTCCAGCAAGAAATTTGTATACACACGTTTGAGACG	720							
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Db 1141 GAACAAACCAAGACCAACAGTGAACAAATGGACAAATGGACA 1183

RESULT 7
AX207388
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Plowman, G., Whyte, D., Manning, G., Sudarsanam, S., and Martinez, R.
Human protein kinases and protein kinase-like enzymes
JOURNAL
Patent: WO 0155356-A 1 02-AUG-2001;
Sugen, Inc. (US)
FEATURES
Location/Qualifiers
1..1594
/organism="Homo sapiens"
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Query Match 95.2%; Score 1165.4; DB 6; Length 1594;
Best Local Similarity 99.1%; Pred. No. 2.2e-295;
Matches 1172; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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Db 404 ATGGGAGCCACACTTCAAGAAAACCCACGCTGTTTGTATGAAATGAAGATGTCACACTTT 463
QY 61 GACCACTTTGAAATTTTGGCGAGCCATTTGGGAAAGGCGATTTTGGGAAAGGTCTGCATTGTA 120
Db 464 GACCACTTTGAAATTTTGGCGAGCCATTTGGGAAAGGCGATTTTGGGAAAGGTCTGCATTGTA 120
QY 121 CAGAAGATGATACCAAGAGATGTACGCAATGAGTACATGATTAACAAAGATGCGGTG 180
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LOCUS
DEFINITION
ACCESSION
VERSION
Sequence 44 from Patent WO0218557.
AX766348
AX766348.1 GI:32260298
PAT 25-JUN-2003
linear
1594 bp
DNA
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LOCUS	AX320936	1191 bp	DNA linear PAT 14-DEC-2001			
DEFINITION	Sequence 3 from Patent WO0181589.					
ACCESSION	AX320936					
VERSION	AX320936.1	GI:17902482				
KEYWORDS	Homo sapiens (human)					
SOURCE	Homo sapiens					
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE	1 Meyers, R. and Hunter, J.J.					
AUTHORS	14911 novel protein kinase molecules and uses therefor					
TITLE	Patent: WO 0181589-A 3 01-NOV-2001.					
JOURNAL	Millennium Pharmaceuticals, Inc. (US)					
FEATURES	Location/Qualifiers					
	source 1..1191					
ORIGIN						
Query Match 95.1%; Score 1163.8; DB 6; Length 1191;						
Best Local Similarity 99.0%; Pred. No. 5.7e-295;						
Matches 1171; Conservative 0; Mismatches 12; Indels 0; Gaps 0;						
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QY	121	CAGAAGATGATACCAAGAGATGTACCGAATGAAGTACATGAATATAACAAAGTCGGTG	180			
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RESULT 10
AX320934
LOCUS

AX320934 1281 bp DNA linear PAT 14-DEC-2001

DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

Sequence 1 from Patent WO0181589.
AX320934
AX320934.1 GI:17902480
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Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
Meyers, R. and Hunter, J.J.
14911 novel protein kinase molecules and uses therefor
Patent: WO 0181589-A 1 01-NOV-2001;
Millennium Pharmaceuticals, Inc. (US)
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CDS

Query Match 95.1%; Score 1163.8; DB 6; Length 1281;
Best Local Similarity 99.0%; Pred. No. 5.7e-295;
Matches 1171; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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QY 421 CGCATCATTCACAGGATATGAAGCTGTGATATTTACTTGTGAGAGACATGTTTCATG 480
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ACCESSION AR432044
VERSION AR432044.1 GI:40194241
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS Ye,J., Yan,C., Di Francesco,V. and Beasley,E.M.
TITLE Isolated human kinase proteins
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DEFINITION Sequence 231 from Patent EP1347046.
ACCESSION AR433107
VERSION AR433107.1 GI:39919242
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S., Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R., Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and Masuko,Y.
TITLE Full-length cDNA sequences
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FEATURES Research Association for Biotechnology (JP)
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Qy	721	ACTGTTGTAACTTACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	780
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Qy      781  CTCGAACCTAATCCAGACCACCAAGATTTTCTCAGTTATCTGTGATGTCAGAACTTCCCGTAT 840
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Job time : 3718 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 20, 2004, 04:12:57 : Search time 2949 Seconds
(without alignments)
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Scoring table: IDENTITY NUC
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Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_est2:*
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8: gb_gse1:*
9: gb_gse2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	948.6	77.5	2477	3 AK044474	AK044474 Mus muscu
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5	556.8	45.5	3439	3 AK082468	AK082468 Mus muscu
6	555.2	45.4	1245	9 AY406286	AY406286 Mus muscu
7	542.4	44.3	1245	9 AY406284	AY406284 Homo sapi
8	535.4	43.7	1245	9 AY406285	AY406285 Pan trogl
9	497.6	40.7	2161	3 AK046439	AK046439 Mus muscu
10	484.8	39.6	1907	3 CR595271	CR595271 full-leng
11	465.6	38.0	829	5 BU156055	BU156055 AGENCOURT
12	457.4	37.4	836	5 BU412592	BU412592 603155332
13	426.4	34.8	869	4 BG033516	BG033516 602302120
14	423.2	34.6	1072	4 BM908009	BM908009 AGENCOURT
15	408.8	33.4	724	6 CR522564	CR522564 UI-M-GHO-
16	392	32.0	711	6 CA320851	CA320851 UI-M-GHO-
17	378	30.9	1003	5 BU146507	BU146507 AGENCOURT
18	375.8	30.7	922	5 BX401698	BX401698 BX401698
19	375.2	30.7	648	6 BY726568	BY726568 BY726568
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39	290.8	23.8	725	6 CD578874	CD578874 UI-M-GMO-
40	284	23.2	788	7 CR629667	CR629667 DKF2p469P
41	283.4	23.2	672	5 BX917647	BX917647 BX917647
42	282.2	23.1	626	6 CA327599	CA327599 UI-M-FYO-
43	276.2	22.6	691	7 CN457090	CN457090 UI-M-HNO-
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ALIGNMENTS

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LOCUS	Mus musculus	7 days neonate cerebellum cDNA, RIKEN full-length		
DEFINITION	enriched library, clone:A73009C22 product:SIMILAR TO SERINE THREONINE KINASE 32 homolog [Homo sapiens], full insert sequence.			
ACCESSION	AK042599.1	GI:26335202		
VERSION	HTC; CAP trapper.			
KEYWORDS	Mus musculus (house mouse)			
SOURCE	Mus musculus			
ORGANISM	Mus musculus			
REFERENCE	1			
AUTHORS	Carninci, P. and Hayashizaki, Y.			
TITLE	High-efficiency full-length cDNA cloning			
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)			
MEDLINE	99279253			
PUBMED	10349636			
REFERENCE	2			
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.			
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes			
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)			
MEDLINE	20499374			
PUBMED	11042159			
REFERENCE	3			
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.			
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer			
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)			
MEDLINE	20530913			
PUBMED	11076861			
REFERENCE	4			
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.			
TITLE	Functional annotation of a full-length mouse cDNA collection			
JOURNAL	Nature 409, 685-690 (2001)			
REFERENCE	5			
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research			

RESULT 2
AK044474
LOCUS
DEFINITION
Mus musculus adult retina cDNA, RIKEN full-length enriched library,
clone: A930015B13 product: SIMILAR TO SERINE THREONINE KINASE 32
homolog (Homo sapiens), full insert sequence.
AK044474
VERSION
AK044474.1 GI:26336516
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1
Carninci, P. and Hayashizaki, Y.
TITLE
High-efficiency full-length cDNA cloning
JOURNAL
Meth. Enzymol. 303, 19-44 (1999)
MEDLINE
99279253
PUBMED
10349636
2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL
Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE
20499374
PUBMED
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3
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multipipillary sequencer
JOURNAL
Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE
20530913
PUBMED
11076861
4
The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
TITLE
Functional annotation of a full-length mouse cDNA collection
JOURNAL
Nature 409, 685-690 (2001)
REFERENCE
5
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
TITLE
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
JOURNAL
Nature 420, 563-573 (2002)
REFERENCE
6
(bases 1 to 2477)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hasegaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
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Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
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Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
TITLE
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)

COMMENT
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Retina RNA was provided by Dr. Stefano Gustinich (Department of
Neurobiology, Harvard Medical School, 220 Longwood Ave., Boston, MA
02115, USA) whose assistance is gratefully acknowledged. Please
visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/.

FEATURES
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evidence: FASTY, 95.5%ID, 94.5%length, match=471)
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QNNNL"

ORIGIN

Query Match 77.5%; Score 948.6; DB 3; Length 2477;
Best Local Similarity 88.8%; Pred. No. 4.5e-252;
Matches 1026; Conservative 0; Mismatches 129; Indels 0; Gaps 0;
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Db 252 ATGGAGGCCACACTTCAAGCAAAGCCACAGTGTGTGATGAAATGAAGATGTCACATTT 311
Qy 61 GACCACCTTGAATTTTGGAGCCATTGGGAAAGGCAGTTTGGAGAGGCTGCATTTGTA 120
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Qy 121 CAGAAAGATGATCAAGAAAGATGTACCAATGAAGTACATGAATAAACAAAAGTGCCTG 180
Db 372 CGGAAGATGATCAAGAAAGATGTACCAATGAAGTACATGAATAAACAAAAGTGCCTG 431
Qy 181 GAGCGCAATGAAGTGAAGAAATGTCTTCAAGAACTCCAGATCATGCGGGTCTGAGGAC 240
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Qy 241 CCTTCTCGGTAAATTTGTGTGATTCCTTCAAGATGAGGAAGATGTCATGTTGTTG 300
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Db 612 GACACAGTGAAGCTCTTCACTGTGAGTGTGTGATGCGCCCTGGAATCCTCGAGAAC 671
Qy 421 CGCATCATTCACAGGATATGAAGCTGACAAATATTTTACTTGGACGAACATGGGCACTG 480

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Qy 541 GCTGCGACCAAGCCTTACATGCGCACCTGAGATGTTTCAGCTCCAGAAAAGGACAGGCTAT 600
Db 792 GCTGCGACCAAGCCTTACATGCGCACCGGAGATGTTTCAGCTCCAGAAAAGGACAGGCTAT 851
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Db 852 TCCTTTGCTGTTGACTGTTGCTGCTGCGAGTGACGGATATGAACTCTCAGAGGCCGG 911
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Db 912 AGACCATATCATATTCGCTCCAGTACTTCCAGCAAGGAAATTTGACATGTTTGAGACA 971
Qy 721 ACTGTTGTAACCTTACCCTTCTGCTGCTGTCACAGGAAATGGTGTCACTTCTTAAAGCTA 780
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Db 1032 CTTGAACCTATTCAGACCAAGATTTCTGATGATCTGATGTCAGCAACTTCCCGTAT 1091
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Qy 1141 GAACAAACCAAGAC 1155
Db 1392 GAACAAACCAAAAC 1406

RESULT 3
AK036266
LOCUS
DEFINITION
Mus musculus 16 days neonate cerebellum cDNA, RIKEN full-length
enriched library, clone:9630050F05 product:SIMILAR TO SERINE
THREONINE KINASE 32 homolog [Homo sapiens], full insert sequence.
ACCESSION
AK036266
VERSION
AK036266.1 GI:26331271
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1
REFERENCE
Carninci, P. and Hayashizaki, Y.
TITLE
High-efficiency full-length cDNA cloning
JOURNAL
Meth. Enzymol. 303, 19-44 (1999)
MEDLINE
99279253
PUBMED
10349636
2
REFERENCE
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Carninci, P., Hayashizaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
JOURNAL
20499374
PUBMED
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3
Shibata, K., Itoh, M., Aizawa, K., Nagasaka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kiteunai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
JOURNAL
20530913
PUBMED
11076861
4
The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
TITLE
Functional annotation of a full-length mouse cDNA collection
NATURE 409, 685-690 (2001)
JOURNAL
5
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
TITLE
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
NATURE 420, 563-573 (2002)
JOURNAL
6 (bases 1 to 3766)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saitoh, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan [E-mail:genome-res@gsc.riken.jp,
URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216]
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/
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evidence: FASTV, 95.5%ID, 94.5%length, match=471)

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GNNNL"
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ORIGIN

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Query Match 77.5%; Score 948.6; DB 3; Length 3766;
Best Local Similarity 88.8%; Pred. No. 5.1e-252;
Matches 1026; Conservative 0; Mismatches 129; Indels 0; Gaps 0;

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QY 181 GAGCGCATGAAGTGAAGAAATGCTTCAAGAACTCCAGATCATGCGGGTCTGGAGC 240
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DB |||||
QY 543 GACCTCTCTCGTGGTGGAGTCACTGCTGATCACTGCAACAGAAAGTCCACTTCAAGAA 602
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DB |||||
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DB |||||
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DB |||||
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DB |||||
Db 1383 GAACAAACCAAGAC 1397
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RESULT 4

BG036777

LOCUS

DEFINITION

ACCSSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Email: cspbs-remail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki

Toshiyuki and Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM10041 row: h column: 24

High quality sequence stop: 764.

Location/Qualifiers

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(Gcgag); Oligo-dT primed using primer

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insert size 2.5 kb and normalized to ROT 5. This is a

primary library enriched for full-length clones and

constructed using the Cap-trapper method (Carninci, in

preparation). Library constructed by M. Brownstein

(NIH/NHGRI, National Institutes of Health). Note: this


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evidence: BLASTN, 99%, match=1955)"
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ORIGIN

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DEFINITION genomic survey sequence.
ACCESSION AY406286
VERSION AY406286.1 GI:39762260
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 1245)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarimal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferrera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Inferred nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1245)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarimal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferrera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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Best Local Similarity 69.1%; Pred. No. 9.6e-143;
Matches 781; Conservative 0; Mismatches 328; Indels 9; Gaps 2;

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DEFINITION genomic survey sequence.
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VERSION AY406284.1 GI:39762258
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1245)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1245)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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Best Local Similarity 69.1%; Pred. No. 3.5e-139;
Matches 773; Conservative 0; Mismatches 336; Indels 9; Gaps 2;

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RESULT 8
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DEFINITION Pan troglodytes HCM2506 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY406285
VERSION AY406285.1 GI:39762259
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
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1 (bases 1 to 1245)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
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Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
14671302
2 (bases 1 to 1245)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
Location/Qualifiers
source 1..1245
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Query Match 43.7%; Score 535.4; DB 9; Length 1245;
Best Local Similarity 68.2%; Pred. No. 3.1e-137; Mismatches 346; Indels 9; Gaps 2;
Matches 763; Conservative 0;
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Db 601 GGATACTCGTACCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
Qy 655 GGCCGGAGACGCTATCATATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 714
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Qy	28	CCAGTGTTTGATGAAAAATGAAGATGTCAACTTTTGACCACTTTTGAAATTTTTCGGAGCAATT	87
Db	350	CCGATGTTTGTGACGAACAGGAGGACGTGAACCTTTGACCACCTTCAGATTCTGAGAGCAATT	409
Qy	88	GGGAAAGCGCAGTTTTTGGGAAGGCTCTGCATTGTCTACAGAAGAATGATACCAAGAAGATGTAC	147
Db	410	GGGAAAGCGCAGCTTTGGCAAGTGTGCATCTGTGCAAGAGCGGACACAGAGAAGATGTAC	469
Qy	148	GCAATGAAGTACATGAATATAACAAAAGTGCCTGGAGCGCAATGAAGTGAAGAAATGTCTTC	207
Db	470	GCCATGAAGTACATGAACAAGCAACAATGCATAGAGCGGATGAGGTCCGGAATGTCTTTC	529
Qy	208	AAGAACTCCAGATCATGCAGGCTCTGGAGACACCTTTCTTGTTAAATTTGTGGTATTC	267
Db	530	CGGAGCTGGAGATCTTACAGGAATCGAGCATCTTCTCTGTGTGAACCTCTGTGTACTCC	589
Qy	268	TTCCAAGATGAGGAAGACATGTTCAATGGTGTGTGACCTCTCTGTGGGTGGAGACCTCGCT	327
Db	590	TTCCAGGATGAGGAGGACATGTTCAATGGTGTGTGATCTGTCTTCTGGGGGAGACCTCGGC	649
Qy	328	TATCACCTGCACAAAGACGTCCACTTTCAAGGAAGAAAAAGTGAAGCTCTTTCATCTGTGAG	387
Db	650	TACCACCTACAGCAGAAATGTTCCAGTCTTCTACAGGACACAGTGAAGCTGTACATCTGTGAG	709
Qy	388	CTGCTCATGGCCCTGGACTACTCTCCAGAACAGGCGCATCATTCACAGGATATGAAGCCT	447
Db	710	ATGGCCCTGGCCCTGSACTACCTCGGTAGCCAAACACATCATCCACAGAGATGTCAAGCCT	769
Qy	448	GACAAATATTTTACTTGTACGAACATGGGCACGTGCACATCACAGATTTTCAACATTTGCTGG	507
Db	770	GACAAACATCTCTCTGGATGAACAGGACATGCACACCTTACTGACTTCAACATTTGCCACC	829
Qy	508	ATGCTGCCAGGGAGACAGATTTACCAACATGGCTGGCACCAAGCTTTACATGGCACCT	567
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Qy	568	GAGATGTTACGCTC-----CAGAAAAGGACAGGCTATTCTTTGCTGTTGACTGTGGTGG	621
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Qy	622	TCCCTGGGAGTGACGGCATATGAACCTGCTGAGAGCCGGAGACCGTATCATATTTCGCTCC	681
Db	950	TCGCTGGGGTGTATGGCTTACGAGCTGCTACGAGATGGAGACCTACGATATCCACTCG	1009
Qy	682	AGTACTTCCACGAAGGAAATTTGTATACACGTTTGGAGCAGCTGTTGTAACTTACCTTCT	741
Db	1010	AGCAATGCTGTGGAGTCCGCTGGTTTTCAGCTGTTTCAGCACTGTGAGTGTCCAGTACGTGCC	1069
Qy	742	GCCTGGTTCACGAAATGGTGTCACTTCTTAAAAGCTACTCGAACCTTAATCCAGACAA	801
Db	1070	ACCTGGTCCAAGGAGATGGTAGCCCTGCTGCGAAAGCTCTTCAACCGTGAACCCCTGAGCAC	1129
Qy	802	CGATTTTCTCAGTTTATCTGATGTCCAGAACTTCCCGTATATGAATGATATAAACTGGGAT	861
Db	1130	CGGTTCTCCAGCTCTCCAAGACATGCAGACAGCCCCCATCGCTGGCCCCAGCTGTGGGAC	1189
Qy	862	GCAATTTTTCAGAGAGGCTCATTTCCAGGTTTTCATTTCTAATAAGGACGAGCTGAATGT	921
Db	1190	GACCTGATGAAAAAGAGGTGGAGCCAGGCTTTGTGCCCCAATAAAGGCGGCTGCACTGT	1249
Qy	922	GATCCTACCTTTGAATCTGAGGAATGATTTTGGAGTCCAAACCTCTACATAGAAAAAA	981
Db	1250	GATCCCACCTTTTGAGCTGGAGGATGATCTCTGAGTCGAGGCTCTGCAACAAGAGAAA	1309
Qy	982	AAGCGTCTGGCAAGAGGAGGATATGAGGAAATCCGCAATTTCTTCAGACATGTCTT	1041
Db	1310	AAGCGCTGGCCAAGATAAGTCTTCGGACACAGCAGAGACAGTTCCTCCAGTCGAGAA	1369
Qy	1042	-----CTTCAAGACCACTTGACTCTGTTCAGAAAGGATTTCAATTTTCAACAGAGAA	1095
Db	1370	GACTACCTGCAAGACTGCTGGATGCCATTCAGCAAGACTTCGTGATTTTAAACAGAGAA	1429

QY	1096	AAGTAAACAGG	1107
Db	1430	AAGTTGAAGG	1441
RESULT 10			
CRS95271		1907 bp mRNA linear HTC 21-JUL-2004	
LOCUS		full-length cDNA clone CS0DL006YN16 of B cells (Ramos cell line)	
DEFINITION		Cot 25-normalized of Homo sapiens (human).	
ACCESSION		CRS95271	
VERSION		CRS95271.1 GI:50476078	
KEYWORDS		HTC; CNSLT_CDNA.	
SOURCE		Homo sapiens (human)	
ORGANISM		Homo sapiens	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
TITLE		1 (bases 1 to 1907)	
JOURNAL		Li W.B., Gruber C., Jesse J. and Polaves D.	
REMARK		Full-length cDNA libraries and normalization Unpublished Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue 2 (bases 1 to 1907) Genoscope. Direct Submission Submitted (20-JUL-2004) Genoscope - Centre National de Sequences ; BP 191 91006 EVRY cedex - FRANCE (E-mail : seoref@genoscope.cns.fr - Web : www.genoscope.cns.fr) 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoK V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. Location/Qualifiers 1..1907 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="CS0DL006YN16" /tissue_type="B cells (Ramos cell line) Cot 25-normalized" /plasmid="pCMVSPORT_6"	
FEATURES			
source			
ORIGIN			
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Matches		728; Conservative 0; Mismatches 352; Indels 12; Gaps 2;	
QY	28	CCAGTGTTTCATGNAATGAAGATGTCACTTTGGACCACCTTGCACCTTTGCGGCCATT	87
Db	168	CCGTGTGTTTACGACAAGGAGGACGTGAACCTTGACCACTTCCAGATCCTTCGGGCCATT	227
QY	88	GCGAAGCGCACGTTTTGGGAAGGCTCTGCATTTGTACAGAAGTAATGATACCAAGAAGATGTAC	147
Db	228	GGGAAGGCGCAGCTTTGGCAAGTGTGCATTTGTCAGAAGCGGCACGGAGAAGATGTAC	287
QY	148	GCAATGAAGTACATGAATAAACAAAAGTCGTGGAGCGCAATGAAGTAGAATAATGCTTC	207
Db	288	GCCATGAAGTACATGAACAAGACGACGTGATCGAGCGCGACGAGGTCCGCAACGCTTTC	347
QY	208	AAGGAATCCAGATCATGAGGGTCTGGACACCCCTTTCCTGGTTAATTTGCTATTCC	267
Db	348	CGGAGCTTGGAGATCCTGCAAGGAGATCGAGACAGCTTCTCTGGTGAACCTCTGGTACTCC	407
QY	268	TTCCAAGATGAGGAAGACATGTTTCATGGTGGTGACCTCTCTGGTGGTGAGACCTGCGT	327
Db	408	TTCCAGGACGAGGAGGACATGTTTCATGGTCTGTGACCTGTACTTGGSCGGGACCTGCGC	467
QY	328	TATCACCTGCAAAGAACGTCCTTCAAGGAAGAAACAGTGAAGCTCTTCTCTGTGTAG	387
Db	468	TACCACCTGCAGAGAACGTCGAGTTCTCCAGAGACACGCTGAGGCTGTATCATCTCGAG	527

388 CTGTCATGCGCCCTGAGTACTCTGCAGAAACGAGCCATCATTCACAGGATATGAAGCCT 447
Db |||||
528 ATGGCACTGGCTCTGAGTACTCTGCGCGCCAGCACATCATCCACAGAGATGTCAAGCCT 587
Qy |||||
448 GACATATTTTACTTGAACATGCGGACGCTGCACATCAGATTTCAACATTTGCTGG 507
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Db |||||
708 GAGATCTTTCCACTCTTTTGTCAAACGCGGGACCGGCTACTCTCTTCGAGGTGACTGGTG 767
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622 TCCCTGGAGTACCGGCAATATGAATCTGAGAGCCGAGACCGTATCATATTGCTGCC 681
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768 TCGGTGGGGGTGATGGCTATGAGCTGCTGCGAGATGAGGCGCCCTATGACATCCACTCC 827
Qy |||||
682 AGTACTTCCAGCAAGGAAATGTACACACGTTTGAGACGACTGTTGTAACTTACCTTCT 741
Db |||||
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742 GCCTGGTACAGGAAATGCTGCTACTTTAAAGCTACTCGAACCTTAATCCAGACCAA 801
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Db |||||
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RESULT 11
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LOCUS AGENCOURT_7970922 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6163821
DEFINITION 5', mRNA sequence.
ACCESSION BU156055
VERSION BU156055.1 GI:22669587
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 829)
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
Plate: L14M13519 row: o column: 22
High quality sequence start: 7
High quality sequence stop: 465.
FEATURES
Location/Qualifiers
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/notes="Organ: Skin; Vector: pCMV-SPORT6; Site: 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 2 kb. Library constructed by Life Technologies."
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Query Match 39.0%; Score 465.6; DB 5; Length 829;
Best Local Similarity 99.2%; Pred. No. 7.1e-118;
Matches 468; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 ATGGAGCCACACTTCAAGAAACACCACTGTTTCATGAAATGAAGATGTCAACTTT 60
Db |||||
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Qy 121 CAGAAGATGATACCAAGAGATGTACGCAATGAAGTACATGAATAAACAAGATGGGTG 180
Db |||||
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Qy 181 GAGCGCAATGAAGTGAAGATGTTTCAAGGAACCTCCAGATCATGCAAGGTTCTGGAGCAC 240
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433 GAGCGCAATGAAGTGAAGATGTTTCAAGGAACCTCCAGATCATGCAAGGTTCTGGAGCAC 492
Qy 241 CTTTCTCTGTTAATTTTGTGTTATCTTCAAGATGAGGAAGATGTTTCATGTTGGTGTG 300
Db |||||
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Qy 301 GACCTCTCTGTTGAGACCTGCGTTATCACTGCAACAGAACGTTCCACTTCAAGGAA 360
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553 GACCTCTCTGTTGAGACCTGCGTTATCACTGCAACAGAACGTTCCACTTCAAGGAA 612
Qy 361 GAAACAGTGAAGCTTTCATCTGTGAGCTGTGATGCCCTGAGTACCTGCGAAGACCA 420
Db |||||
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Qy 421 CGCATCATTCACAGGATGAGCCCTGACAAATATTTTACTTGCAGAACATG 472
Db |||||
673 CGCATCATTCACAGGATGAGCCCTGACAAATATTTTACTTGCAGAACATG 724

RESULT 12
BU412592 836 bp mRNA linear EST 29-NOV-2002
LOCUS BU412592
DEFINITION 603155332F1 CSEORBL05 Gallus gallus cDNA clone CHEST168p8 5', mRNA sequence.
ACCESSION BU412592
VERSION BU412592.1 GI:25905263
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Gallus.
BU412592 836 bp mRNA linear EST 29-NOV-2002
603155332F1 CSEORBL05 Gallus gallus cDNA clone CHEST168p8 5', mRNA sequence.
BU412592
BU412592.1 GI:25905263
EST.
Gallus gallus (chicken)
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Gallus.

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 724)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Dr. Jm Lin, University of Iowa
cDNA library preparation: Dr. M. Bento Soares, University of Iowa
CDNA library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/mousefl.html>
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)

Seq primer: pYX-5,
Location/Qualifiers
1. .724
/organism="Mus musculus"
/mol_type="mRNA"
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/dev_stage="1, 5, and 15 days newborn"
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/note="Organ: Brain; Vector: pYX- Asc; Site 1: Ecor I;
Site 2: Not I; The library was constructed according
Bonafdo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose,
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with Ecor I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CGAATGTAAT. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."

FEATURES
source

ORIGIN

Query Match	33.4%	Score	408.8	DB	6	Length	724
Best Local Similarity	85.5%	Pred. No.	4.3e-102				
Matches	455	Conservative	0	Mismatches	77	Indels	0
Gaps	0						
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Qy	684	TACTTCCAGCA	AGGAATTTGTACACAGTTTGAGACGACTGTTCTAACTTACCCCTTCGC	743			
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Db	129	CTGGTCA	CAGAGATGGTGATCCCTTCTTAAAGCTGCTTGAACCTTAATCCAGACCAACG	188			
Qy	804	ATTTTCTCAG	TATCTGATGCCAGACTTCCCGTATATGAATCATATAAATCGGATGC	863			
Db	189	CTTTTCTCAG	TCTGACTGACATTCAGAAATTTCCCTTACATGAGTGACATGAATCGGACGC	248			
Qy	864	AGTTTTT	CAGAAGGCTCATTTCCAGGTTTCATTTCTTAATAAAGCGCGGCTGAATTGTGA	923			
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Qy	924	TCCTACCTTT	GAACTTGAGGAATGATTTTGGAGTCCAAACCTCTACATAAGAAAAAAA	983			
Db	309	CCCCACTTT	TGAACTCGAAGAAATGATTTTGGAGTCCAAACCTCTTACAGAAAAAGAA	368			

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 17, 2004, 09:25:19 ; Search time 70 Seconds
(without alignments)
2085.755 Million cell updates/sec

Title: US-10-620-845-9

Perfect score: 2151

Sequence: 1 MGANTSRRKPPVDENEDVNF.....VTNGQMDTGLSETFTQTSKVS 407

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004as:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	2060	95.8	396	AAE14261	Aae14261 Novel hum
4	2060	95.8	396	AAE21725	Aae21725 Human PKI
5	2054	95.5	396	AAE50334	Aam50334 Human 149
6	2054	95.5	396	ADL27077	Adl27077 Protein o
7	2047	95.2	396	ABG70700	Abg70700 Human ser
8	2047	95.2	396	ABU62276	Abu62276 Human kin
9	2047	95.2	396	ADL09162	Adl09162 Human pro
10	1880	87.4	398	ADF44523	Adf44523 Mouse kin
11	1875	87.2	398	ADF44527	Adf44527 Mouse kin
12	1827	84.9	358	ADM03989	Adm03989 Human pro
13	1513.5	70.4	327	AAU03504	Aau03504 Human pro
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15	1430.5	66.5	404	ADL09164	Adl09164 Mouse ser
16	1423.5	66.2	403	ABU62278	Abu62278 Human ser
17	1423.5	66.2	403	ADL09165	Adl09165 Human ser
18	1423.5	66.2	414	ABE5600	Abe5600 Novel pro
19	1423.5	66.2	414	ABP43807	Abp43807 Serine/th
20	1423.5	66.2	414	AAO17710	Aao17710 Human ser
21	1423.5	66.2	414	ABE58617	Abe58617 Human can
22	1423.5	66.2	414	ABE38375	Abe38375 Human pro
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ALIGNMENTS

RESULT 1

AAE14260

ID AAE14260 standard; protein; 407 AA.

XX AAE14260;

XX AC

XX 07-MAR-2002 (first entry)

XX DE

XX Novel human protein (NHP) kinase #3.

XX KW

XX Novel human protein; NHP; gene therapy; diagnosis; drug screening;

XX KW gene expression; breast cancer; prostate cancer; nutraceutical; cosmetic;

XX KW medical disorder; mental; biological; physiological; chemotherapeutic.

XX OS

XX Homo sapiens.

XX PN

XX WO200181557-A2.

XX PD

XX 01-NOV-2001.

XX XX

XX 24-APR-2001; 2001WO-US013149.

XX PR

XX 25-APR-2000; 2000US-0199499P.

XX PR

XX 01-MAY-2000; 2000US-0201227P.

XX FA

XX (LEXI-) LEXICON GENETICS INC.

XX PI

XX Hu Y, Nepomniichy B, Wang X, Donoho G, Scoville J, Walke DW;

XX XX

XX WPI; 2002-034442/04.

XX DR

XX N-PSDB; AAD23678.

XX DR

XX New nucleic acid molecules encoding new human proteins, useful in

XX PT diagnosis, drug screening, clinical trial monitoring, treatment of

XX PT physiological disorders, and cosmetic or nutraceutical applications.

XX XX

XX Claim 5; Page 41-42; 44pp; English.

XX PS

XX The invention relates to novel human protein (NHP) kinases and their

XX XX corresponding cDNA molecules. NHP kinase and its DNA are useful as

XX CC reagents in assays for screening compounds that can be used as

XX CC pharmaceutical reagents useful in the therapeutic treatment of mental,

XX CC biological and medical disorders, and also as chemotherapeutic agents

XX CC useful in the treatment of breast cancer and prostate cancer. NHP DNA is

XX CC useful for diagnosis, drug screening, clinical trial monitoring, the

XX CC treatment of physiological disorders or diseases, and cosmetic and

XX CC nutraceutical applications. NHP DNA is also useful for the identification

XX CC of coding sequence and the mapping of a unique gene to a particular

CC chromosome. NHP DNA is further useful as hybridisation probes for
 CC screening libraries and assessing gene expression patterns, and also for
 CC the detection of mutant NHPs or inappropriately expressed NHPs for
 CC disease diagnosis. NHP DNA is also useful in gene therapy. The present
 CC sequence is novel human protein (NHP) kinase which is similar to
 CC serine/threonine protein kinases, ribosomal protein kinases and cAMP-
 CC dependent kinases related to the invention

XX SQ Sequence 407 AA;

Query Match 100.0%; Score 2151; DB 5; Length 407;
 Best Local Similarity 100.0%; Pred. No. 9.4e-196;
 Matches 407; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGANTSRRKPPVFDENEDVNFDFEILRAIGKSGFGKVCIVQKNDTKQYAMKYNKQKCV 60
 Db 1 MGANTSRRKPPVFDENEDVNFDFEILRAIGKSGFGKVCIVQKNDTKQYAMKYNKQKCV 60
 Qy 61 ERNEVRNVFKELQIMQGLEHPLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120
 Db 61 ERNEVRNVFKELQIMQGLEHPLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120
 Qy 121 ETVKLFICELVMDLYLQONRIIHRDKPDNILLDEHGHVHTDFNIAAMLPRETQITTM 180
 Db 121 ETVKLFICELVMDLYLQONRIIHRDKPDNILLDEHGHVHTDFNIAAMLPRETQITTM 180
 Qy 181 AGTKPYMAPEFSSRKAGYGFVDMWSLGVYAYELLGRPPYHRSSTSSKEIVHVFET 240
 Db 181 AGTKPYMAPEFSSRKAGYGFVDMWSLGVYAYELLGRPPYHRSSTSSKEIVHVFET 240
 Qy 241 TVVTYPSAWSQEWMSLLKLEPNPDQRFSLSDVQNPFPYNDINWDAVFQKRLIPGIP 300
 Db 241 TVVTYPSAWSQEWMSLLKLEPNPDQRFSLSDVQNPFPYNDINWDAVFQKRLIPGIP 300
 Qy 301 NKGRNLCDPTFELEEMILESPLHKKKRLAKKEDMKKCDSSQTCLLQEHLDVSQKEFI 360
 Db 301 NKGRNLCDPTFELEEMILESPLHKKKRLAKKEDMKKCDSSQTCLLQEHLDVSQKEFI 360
 Qy 361 IFNREKVNDRFNKROPNLALQTKDPQVTNGQMDTGLSETFTQTSKVS 407
 Db 361 IFNREKVNDRFNKROPNLALQTKDPQVTNGQMDTGLSETFTQTSKVS 407

RESULT 2
 AAB85491
 ID AAB85491 standard; protein; 396 AA.

XX AC AAB85491;

XX DT 25-SEP-2001 (first entry)

XX DE Human protein kinase SGK177.

XX KW Protein kinase; enzyme; cytostatic; neurotropic; neuroprotective; human;
 KW antiparkinsonian; virucide; antibacterial; antifungal; antimigraine;
 KW analgesic; hypotensive; hypertensive; immunosuppressive; antiallergic;
 KW antipsoriatic; antineumatic; antiarthritic; ophthalmological; anorectic;
 KW osteoporotic; thrombolytic; antiarteriosclerotic; antiasthmatic;
 KW vasotrophic; antidiabetic; gene therapy.

OS Homo sapiens.

XX PN WO200155356-A2.

XX PD 02-AUG-2001.

XX PF 25-JAN-2001; 2001WO-US002337.

XX PR 25-JAN-2000; 2000US-0178078P.

XX PR 31-JAN-2000; 2000US-0179364P.

XX PR 17-FEB-2000; 2000US-0183173P.

XX PR 17-MAR-2000; 2000US-0190162P.

XX PR 29-MAR-2000; 2000US-0193404P.

PR 13-NOV-2000; 2000US-0247013P.

XX PA (SUGE-) SUGEN INC.

XX PI Plowman G, Whyte D, Manning G, Sudarsanam S, Martinez R;

XX DR WPI; 2001-476202/51.

XX DR N-PSDB; AAH46891.

XX Kinase polypeptides useful for treating cancers, Alzheimer's disease,
 PT viral infections, diabetes, obesity, organ transplant rejection and
 PT rheumatoid arthritis.

PS Claim 7; Page 214; 218pp; English.

XX The invention provides human protein kinases and protein kinase-like
 CC enzymes and polynucleotides encoding the polypeptides. The kinase
 CC polypeptides and their modulators are useful for treating a disease or
 CC disorder such as cancer, immune-related diseases, cardiovascular disease,
 CC brain or neuronal-associated disease and metabolic disorders, including
 CC cancers of tissues, cancers of hematopoietic origin, diseases of the
 CC central nervous system, diseases of the peripheral nervous system,
 CC Alzheimer's disease, Parkinson's disease, multiple sclerosis, amyotrophic
 CC lateral sclerosis, viral infections, infections caused by prions,
 CC bacteria and fungi, ocular diseases, migraines, pain, sexual dysfunction,
 CC mood disorders, attention disorders, cognition disorders, hypotension,
 CC hypertension, psychotic disorders, neurological disorders, dyskinesias,
 CC metabolic disorders, and organ transplant rejection. They are also useful
 CC for treating rhinitis, autoimmunity, atherosclerosis, psoriasis,
 CC osteoarthritis, asthma, chronic inflammatory pelvic disease, chronic
 CC inflammatory bowel disease, rheumatoid arthritis, metabolic disorders
 CC such as diabetes, obesity, cardiovascular diseases such as reperfusion
 CC injury, coronary thrombosis, clotting disorders and atherosclerosis,
 CC ocular diseases such as glaucoma, retinopathy and macular degeneration,
 CC psychiatric and neurological disorders such as anxiety, schizophrenia,
 CC dementia, manic depression, etc. The polynucleotides are useful in gene
 CC therapy techniques to treat the above mentioned disorders. Sequences
 CC AAB85491-85522 represent the human protein kinases of the invention

XX SQ Sequence 396 AA;

Query Match 95.8%; Score 2060; DB 4; Length 396;
 Best Local Similarity 99.2%; Pred. No. 4.2e-187;
 Matches 389; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MGANTSRRKPPVFDENEDVNFDFEILRAIGKSGFGKVCIVQKNDTKQYAMKYNKQKCV 60

Db 1 MGANTSRRKPPVFDENEDVNFDFEILRAIGKSGFGKVCIVQKNDTKQYAMKYNKQKCV 60

Qy 61 ERNEVRNVFKELQIMQGLEHPLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120

Db 61 ERNEVRNVFKELQIMQGLEHPLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120

Qy 121 ETVKLFICELVMDLYLQONRIIHRDKPDNILLDEHGHVHTDFNIAAMLPRETQITTM 180

Db 121 ETVKLFICELVMDLYLQONRIIHRDKPDNILLDEHGHVHTDFNIAAMLPRETQITTM 180

Qy 181 AGTKPYMAPEFSSRKAGYGFVDMWSLGVYAYELLGRPPYHRSSTSSKEIVHVFET 240

Db 181 AGTKPYMAPEFSSRKAGYGFVDMWSLGVYAYELLGRPPYHRSSTSSKEIVHVFET 240

Qy 241 TVVTYPSAWSQEWMSLLKLEPNPDQRFSLSDVQNPFPYNDINWDAVFQKRLIPGIP 300

Db 241 TVVTYPSAWSQEWMSLLKLEPNPDQRFSLSDVQNPFPYNDINWDAVFQKRLIPGIP 300

Qy 301 NKGRNLCDPTFELEEMILESPLHKKKRLAKKEDMKKCDSSQTCLLQEHLDVSQKEFI 360

Db 301 NKGRNLCDPTFELEEMILESPLHKKKRLAKKEDMKKCDSSQTCLLQEHLDVSQKEFI 360

Qy 361 IFNREKVNDRFNKROPNLALQTKDPQVTNGQ 392

Db 361 IFNREKVNDRFNKROPNLALQTKDPQVTNGQ 392


```
DR WPI; 2002-329769/36.
XX N-PSDB; AAD34317.
XX New human kinases, useful for diagnosing, treating or preventing immune
PT system disorders (e.g. Crohn's disease), neurological disorders (e.g.
PT epilepsy), or cell proliferative disorders (e.g. cancers such as leukemia
PT or lymphoma).
XX
PS Claim 75; Page 184-185; 218pp; English.
XX
CC The present invention relates to human kinases (PKIN) and polynucleotides
CC encoding such proteins. PKIN sequences of the invention are useful for
CC diagnosing, treating or preventing disorders associated with aberrant
CC expression of PKIN, particularly immune system disorders (e.g. acquired
CC immune deficiency syndrome (AIDS), thymic hypoplasia, Crohn's disease,
CC anaemia, asthma), neurological disorders (e.g. epilepsy, Charcot-Marie-
CC Tooth disease or seizures), cell proliferative disorders (e.g. cancers
CC such as adenocarcinoma, leukaemia, lymphoma, melanoma, sarcoma),
CC and developmental disorders (e.g. Down's syndrome). They are also used in
CC gene therapy and protein therapy. The present sequence is human PKIN-20
CC protein
XX
SQ Sequence 396 AA;

Query Match 95.8%; Score 2060; DB 5; Length 396;
Best Local Similarity 99.2%; Pred. No. 4.2e-187;
Matches 389; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGANTSRRPPVDENEDVNFHETLRAIGSGFGKVCIVOKNDTKMYAMKYNKQCV 60
DQ |||||
DQ 1 MGANTSRRPPVDENEDVNFHETLRAIGSGFGKVCIVOKNDTKMYAMKYNKQCV 60
QY 61 ERNEVRNVFKELQIMQGLEHFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQNVHFKE 120
DQ |||||
DQ 61 ERNEVRNVFKELQIMQGLEHFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQNVHFKE 120
QY 121 ETVKLFICELVMALDYLNQRIIHRDMKPDNILLDEHGHVHITDFNTAAMLPRETQITTM 180
DQ |||||
DQ 121 ETVKLFICELVMALDYLNQRIIHRDMKPDNILLDEHGHVHITDFNTAAMLPRETQITTM 180
QY 181 AGTKPYMAPFSSRKAGYGFVDWWSLGVATVELLGRPYHIRSTSKELVHTFET 240
DQ |||||
DQ 181 AGTKPYMAPFSSRKAGYGFVDWWSLGVATVELLGRPYHIRSTSKELVHTFET 240
QY 241 TVVTYPSAWSQEMVSLKLLLEPNPDQRFQSLSDVQNPFPYMNNDINWDVAFQKRLIPGIP 300
DQ |||||
DQ 241 TVVTYPSAWSQEMVSLKLLLEPNPDQRFQSLSDVQNPFPYMNNDINWDVAFQKRLIPGIP 300
QY 301 NKGRLNCDPTELEEMILESPLHKKRKLAKKEDMRKCDSSQTCLLQEHLDVQKEFI 360
DQ |||||
DQ 301 NKGRLNCDPTELEEMILESPLHKKRKLAKKEDMRKCDSSQTCLLQEHLDVQKEFI 360
QY 361 IFNREKVNDRDNKQPNLALBQTKDPQVNTGQ 392
DQ |||||
DQ 361 IFNREKVNDRDNKQPNLALBQTKDPQVNTGQ 392

RESULT 5
AAM50334
ID AAM50334 standard; protein; 396 AA.
XX
AC AAM50334;
XX
DT 04-FEB-2002 (first entry)
XX
DE Human 14911 protein kinase.
XX
KW Protein kinase; human; signal transduction; lung cancer; colon cancer;
KW brain cancer; breast cancer; therapy; diagnosis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
```

```
Modified-site 2..7 /note= "N-myristoylated"
FT FT
Modified-site 4..7 /note= "Asn is N-glycosylated"
FT FT
Modified-site 5..7 /note= "O-phosphorylated by protein kinase C"
FT FT
Domain 23..281 /label= Protein_kinase_domain
FT FT
Peptide 29..37 /note= "protein kinase ATP-binding region signature"
FT FT
Modified-site 43..46 /note= "Asn is N-glycosylated"
FT FT
Modified-site 45..47 /note= "O-phosphorylated by protein kinase C"
FT FT
Modified-site 89..92 /note= "O-phosphorylated by casein kinase II"
FT FT
Modified-site 122..124 /note= "O-phosphorylated by protein kinase C"
FT FT
Active-site 142..154 /note= "active site signal"
FT FT
Modified-site 193..195 /note= "O-phosphorylated by protein kinase C"
FT FT
Modified-site 197..202 /note= "N-myristoylated"
FT FT
Modified-site 212..215 /note= "O-phosphorylated by casein kinase II"
FT FT
Modified-site 218..221 /note= "Aamidated"
FT FT
Modified-site 230..233 /note= "O-phosphorylated by casein kinase II"
FT FT
Modified-site 230..232 /note= "O-phosphorylated by protein kinase C"
FT FT
Domain 282..301 /label= Protein_kinase_C-terminal_domain
FT FT
Modified-site 391..396 /note= "N-myristoylated"
FT FT
WO200181589-A2.
XX
XX
XX 01-NOV-2001.
PD
XX
XX 25-APR-2001; 2001WO-US013785.
PF
XX
XX 25-APR-2000; 2000US-0199391P.
PR
XX 15-JUN-2000; 2000US-00593927.
PR
XX (MILL-) MILLENNIUM PHARM INC.
PA
XX
XX Meyers R, Hunter JJ;
PI
XX
XX WPI; 2002-041408/05.
DR
XX N-PSDB; AAI70704.
DR
XX
XX Novel protein kinase nucleic acid molecules and the encoded proteins for
PT diagnosing and treating cellular proliferative, bone, immune,
PT cardiovascular, liver, pain or metabolic disorders and identifying
PT modulators.
XX
XX Claim 4(d); Fig 1A-B; 115pp; English.
PS
XX
XX The present sequence is that of a novel human protein kinase, designated
CC 14911. This protein kinase plays a role in, or functions in, the
CC transduction of signals for cell proliferation, differentiation and
CC apoptosis, modulating the activity of one or more proteins involved in
CC cellular growth or differentiation. 14911 molecules are overexpressed in
CC some tumour cells, where they may inappropriately propagate either cell
CC proliferation or cell survival signals. The invention provides methods
CC for the diagnosis and treatment of cancer, including breast colon, brain
CC and especially lung cancer (claimed), and methods for evaluating the
CC efficacy of treatment. 14911 polypeptides can be produced by culturing
CC of claimed host cells, and used in claimed methods of identifying 14911
CC modulator compounds. 14911 binding partners are used in claimed methods
CC of identifying subjects at risk of cancer or cellular proliferation
```


CC and/or differentiation disorders. A claimed method of treating cancer or
CC a cellular proliferation and/or differentiation disorder, especially
CC lung, colon, brain and breast cancer, uses a small molecule, peptide,
CC phosphopeptide, anti-14911 antibody, a 14911 polypeptide or its variant.
CC Other disorders that may be diagnosed/treated include those associated
CC with bone metabolism, autoimmune diseases, cardiovascular disorders,
CC liver disorders, viral diseases, pain and metabolic disorders
XX
XX

SQ Sequence 396 AA;

Query Match 95.5%; Score 2054; DB 5; Length 396;

Best Local Similarity 99.0%; Pred. No. 1.6e-186;

Matches 388; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MGANTSRRKPPVFDENEDVNFDFHFEILRAIGKSGFGKVCIVQKNDTKMYAMKYNKQKCV 60

Db 1 MGANTSRRKPPVFDENEDVNFDFHFEILRAIGKSGFGKVCIVQKNDTKMYAMKYNKQKCV 60

Qy 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEDMFMVVDLLGGDLRYHLQONVHFK 120

Db 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEDMFMVVDLLGGDLRYHLQONVHFK 120

Qy 121 ETVKLFCICELVMDLYLQONQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETIQITM 180

Db 121 ETVKLFCICELVMDLYLQONQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETIQITM 180

Qy 181 AGTKPYNAPEMFSSRRKAGYSFAVDWWSLGYATYELLGRPPYHIRSTSKELVHTFET 240

Db 181 AGTKPYNAPEMFSSRRKAGYSFAVDWWSLGYATYELLGRPPYHIRSTSKELVHTFET 240

Qy 241 TVVTYPSAWSQEMVSLKLLPEPNDQRFSDVQNFPPYMNNDINWDAVQKRLPGIP 300

Db 241 TVVTYPSAWSQEMVSLKLLPEPNDQRFSDVQNFPPYMNNDINWDAVQKRLPGIP 300

Qy 301 NKGRLCDPTFELREMIKLEKPLHKKKXKLAKEKDMKCDSSQTCLLQEHLDVQKEFI 360

Db 301 NKGRLCDPTFELREMIKLEKPLHKKKXKLAKEKDMKCDSSQTCLLQEHLDVQKEFI 360

Qy 361 IFNREKVNDRDNKQPNLALEQTKDPQVNTGQ 392

Db 361 IFNREKVNDRDNKQPNLALEQTKDPQGEDQ 392

RESULT 6

ADL27077

ID ADL27077 standard; protein; 396 AA.

AC ADL27077;

XX 20-MAY-2004 (first entry)

DT Protein of novel human molecule, 14911.

XX 26199; 33530; 33949; 47148; 50226; 58764; 62113; 32144; 32235; 23565;
XX 13305; 14911; 86216; 25206; 8843; cytosolic; haemostatic; gynecological;
XX nephrotropic; dermatological; immunosuppressive; antiinflammatory;
XX hepatotropic; virucide; analgesic; vasotropic; gene therapy;
XX cellular proliferative; differentiative disorder; brain; platelet;
XX breast; colon; kidney; lung; ovarian; prostate; haematopoietic;
XX pancreatic; skeletal muscle; skin; bone metabolism; immune;
XX transgenic animal; chromosome identification; tissue typing; human.

XX Homo sapiens.

OS US2004005664-A1.

XX 08-JAN-2004.

XX 10-APR-2003; 2003US-00410764.

XX 25-APR-2000; 2000US-0199391P.

XX 19-MAY-2000; 2000US-0205301P.

XX 15-JUN-2000; 2000US-00593927.

PR 01-SEP-2000; 2000US-0229300P.

PR 05-OCT-2000; 2000US-0238054P.

PR 11-OCT-2000; 2000US-00686673.

PR 30-NOV-2000; 2000US-0250186P.

PR 16-FEB-2001; 2001US-0269440P.

PR 17-MAY-2001; 2001US-00860352.

PR 06-AUG-2001; 2001US-00924358.

PR 24-AUG-2001; 2001US-0314884P.

PR 27-SEP-2001; 2001US-00966614.

PR 29-OCT-2001; 2001US-0347815P.

PR 29-NOV-2001; 2001US-00997816.

PR 24-JAN-2002; 2002US-0351572P.

PR 15-FEB-2002; 2002US-00076535.

PR 23-AUG-2002; 2002US-00226410.

PR 25-OCT-2002; 2002US-00281094.

PR 24-JAN-2003; 2003US-00350553.

XX (MILL-) MILLENNIUM PHARM INC.

XX Meyers RE, Macbeth KJ, Curtis RAJ, Rudolph-Owen LA, Weich NS;

PI Olandt PJ, Tsai F, Kapeller-Libermann R, Carroll JM;

XX WPI; 2004-081724/08.

DR N-PSDB; ADL27076, ADL27078.

XX New isolated 26199, 33530, 33949, 47148, 50226, 58764, 62113, 32144,

PT 32235, 23565, 13305, 14911, 86216, 25206 or 8843 polypeptides and nucleic

PT acids, useful for diagnosing or treating cancer, autoimmune, metabolic

XX and viral diseases.

XX Claim 4; SEQ ID NO 101; 237pp; English.

XX The invention relates to novel nucleic acid molecules designated 26199,

CC 33530, 33949, 47148, 50226, 58764, 62113, 32144, 32235, 23565, 13305,

CC 14911, 86216, 25206 or 8843. The novel nucleic acid molecules and their

CC compositions have the following activities: cytostatic, haemostatic,

CC gynecological, nephrotropic, dermatological, immunosuppressive,

CC antiinflammatory, hepatotropic, virucide, analgesic, and vasotropic. The

CC novel nucleic acid molecules may be used in gene therapy to treat

CC disorders. The methods and compositions of the present invention are

CC useful for the diagnosis, prevention and/or treatment of diseases or

CC polypeptides, such as a cellular proliferative and/or differentiative

CC disorder, brain disorder, platelet disorder, breast disorder, colon

CC disorder, kidney (renal) disorder, lung disorder, ovarian disorder,

CC prostate disorder, haematopoietic disorder, pancreatic disorder, skeletal

CC muscle disorder, skin (dermal) disorder, disorder associated with bone

CC metabolism, immune, e.g., inflammatory, disorder, cardiovascular

CC disorder, endothelial cell disorder, liver disorder, viral diseases, pain

CC disorder, metabolic disorder, neurological or CNS disorder, erythroid

CC disorder or anaemic disorder. The compositions may also be used in assays

CC to identify other proteins or molecules involved in binding reaction, to

CC generate transgenic animals or knockout animals, which in turn are useful

CC in the development and screening of therapeutically useful reagents, for

CC chromosome identification, and tissue typing. This sequence represents a

CC protein derived from one of the novel human nucleic acid molecules of the

CC invention.

XX Sequence 396 AA;

SQ Query Match 95.5%; Score 2054; DB 8; Length 396;

Best Local Similarity 99.0%; Pred. No. 1.6e-186;

Matches 388; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MGANTSRRKPPVFDENEDVNFDFHFEILRAIGKSGFGKVCIVQKNDTKMYAMKYNKQKCV 60

Db 1 MGANTSRRKPPVFDENEDVNFDFHFEILRAIGKSGFGKVCIVQKNDTKMYAMKYNKQKCV 60

Qy 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEDMFMVVDLLGGDLRYHLQONVHFK 120

Db 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEDMFMVVDLLGGDLRYHLQONVHFK 120

Qy 121 ETVKLFCICELVMDLYLQONQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETIQITM 180

Db 121 ETVKLFICELVWALDYLNQRIIHRDMKPDNILLDEHGHVITDNFIAAMLPREIQTITM 180
Qy 181 AGTKPYMAPEMSSRGAGYSAVDWWSLGVTAAYELLGRRRPYHRSSTSSKEIYHTTET 240
Db 181 AGTKPYMAPEMSSRGAGYSAVDWWSLGVTAAYELLGRRRPYHRSSTSSKEIYHTTET 240
Qy 241 TVVTYPSAWSQBMVSLKKLEPNPDQRFSQLSDVQNFYPMNDINWDVAVFQKRLIPGP 300
Db 241 TVVTYPSAWSQBMVSLKKLEPNPDQRFSQLSDVQNFYPMNDINWDVAVFQKRLIPGP 300
Qy 301 NKGRLNCDTPELEWILESKPLHKKRLAKKEDMKRKCDSSTQCLQEHLDVQKXFI 360
Db 301 NKGRLNCDTPELEWILESKPLHKKRLAKKEDMKRKCDSSTQCLQEHLDVQKXFI 360
Qy 361 IFNREKVNDFNKPONLALQETKDPQVYNGQ 392
Db 361 IFNREKVNDFNKPONLALQETKDPQGEDGQ 392
RESULT 7
ID ABG70700
XX ABG70700 standard; protein; 396 AA.
AC ABG70700;
XX
DT 17-JAN-2003 (first entry)
XX
DE Human serine/threonine protein kinase-like kinase.
XX
KW Human; kinase; serine/threonine kinase; immune response; transgenic;
KW enzyme.
XX
OS Homo sapiens.
XX
FH Key
FT Location/Qualifiers
FT 2..7
FT /label= N_myristoylation_site
FT 4..7
FT /label= N_glycosylation_site
FT 5..7
FT /label= Protein_kinase_C_phosphorylation_site
FT 6..8
FT /label= Protein_kinase_C_phosphorylation_site
FT 29..52
FT /label= Protein_kinase_ATP-binding_region
FT 33..36
FT /label= Casein_kinase_II_phosphorylation_site
FT 43..46
FT /label= N_glycosylation_site
FT 45..47
FT /label= Protein_kinase_C_phosphorylation_site
FT 89..92
FT /label= Casein_kinase_II_phosphorylation_site
FT 122..124
FT /label= Protein_kinase_C_phosphorylation_site
FT 142..154
FT /label= Serine/threonine_protein_kinase_active_site
FT 193..195
FT /label= Protein_kinase_C_phosphorylation_site
FT 194..196
FT /label= Protein_kinase_C_phosphorylation_site
FT 197..202
FT /label= N_myristoylation_site
FT 212..215
FT /label= Casein_kinase_II_phosphorylation_site
FT 218..221
FT /label= Amidation_site
FT 230..233
FT /label= Casein_kinase_II_phosphorylation_site
FT 391..396
FT /label= N_myristoylation_site
XX

PN US2002127683-A1.
XX
PD 12-SEP-2002.
XX
PF 09-MAR-2001; 2001US-00801876.
XX
PR 09-MAR-2001; 2001US-00801876.
XX
PA (YEJ/) YE J.
PA (YANC/) YAN C.
PA (DPA/) DI FRANCESCO V.
XX (BEAS/) BEASLEY E M.
PI Ye J, Yan C, Di Francesco V, Beasley EM;
XX
DR WPI; 2003-028938/02.
DR N-PSDB; ABS55499, ABS55500.
XX
PT Novel isolated human kinase peptide useful for treating disorder
PT characterized by absence of, in appropriate or unwanted expression of the
PT kinase protein, and as immunogens to raise antibodies.
XX
PS Claim 1; Fig 2; 174pp; English.
XX
CC The present invention relates to the isolation of a human kinase and the
CC polynucleotide sequences encoding it. The human kinase of the invention
CC is related to the serine/threonine kinase subfamily. The gene encoding
CC the human kinase is located on chromosome 5. The polypeptide and
CC polynucleotide sequences of the invention are useful for treating a
CC disease or condition mediated by a human kinase. Both the polypeptide and
CC polynucleotide sequences are useful as models for the development of
CC human therapeutics, for identifying therapeutic proteins, as targets for
CC development of human therapeutic agents, and as query sequences to
CC perform a search against sequence data bases to identify other family
CC members of related sequences. The polypeptide is useful to raise
CC antibodies or to elicit another immune response, as a reagent in assays
CC designed to quantitatively determine levels of the protein in biological
CC fluids, as markers for tissues in which the corresponding protein is
CC preferentially expressed, in drug screening assays, in cell-based or cell
CC -free systems, to identify compounds that modulate kinase activity of the
CC protein in its natural state, or an altered form that causes the specific
CC disease or pathology associated with the kinase, to screen a compound for
CC the ability to stimulate or inhibit interaction between the kinase
CC protein and a molecule that normally interacts with the kinase protein,
CC and in pharmacogenomic analysis. The polynucleotide is useful for
CC monitoring the effectiveness of modulating compounds on the expression or
CC activity of the human kinase gene in clinical trials or in a treatment
CC regimen, in diagnostic assays for qualitative changes in a human kinase
CC nucleic acid that leads to a pathology, for testing an individual for a
CC genotype that while not necessarily causing a disease, nevertheless
CC affects the treatment modality, as antisense constructs to control human
CC kinase gene expression in cells, tissues and organisms, for gene therapy
CC in patients containing cells that are aberrant in human kinase gene
CC expression, and to produce transgenic animals. The present sequence
CC represents a human kinase related to the serine/threonine protein kinase
CC subfamily
SQ Sequence 396 AA;
Query Match 95.2%; Score 2047; DB 6; Length 396;
Best Local Similarity 98.7%; Pred. No. 7.2e-186;
Matches 387; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Qy 1 MGANTSRKPPVPFEDNEDVNFDFEILRAIGKSGFGKVCIVQKNDTKMYAMKYNKQKV 60
Db 1 MGANTSRKPPVPFEDNEDVNFDFEILRAIGKSGFGKVCIVQKNDTKMYAMKYNKQKV 60
Qy 61 ERNEVERNFKELQIMQGLEHPPFLVNLWYSFQDEDMFMVVDVLLGLGDLRYHLQONVFXE 120
Db 61 ERNEVERNFKELQIMQGLEHPPFLVNLWYSFQDEDMFMVVDVLLGLGDLRYHLQONVFXE 120
Qy 121 ETVKLFICELVWALDYLNQRIIHRDMKPDNILLDEHGHVITDNFIAAMLPREIQTITM 180

Db	121	ETVKLFICELVNALDYLNQRILIHDKMCPNILLDEHGHVHITDNTIAAMLPRETOITTM	180		
Qy	181	AGTKPTMAPEMFSSRRKGAGYGFADVWWSLGVTAAYELLRGRPPYHRSSTSSKEIVHTFET	240		
Db	181	AGTKPTMAPEMFSSRRKGAGYGFADVWWSLGVTAAYELLRGRPPYHRSSTSSKEIVHTFET	240		
Qy	241	TVVTPYSAWSQBMVSLKKLLLEPNPDQFQSLSDVQNPFPYMDINWDVAFQKRLIPGFIP	300		
Db	241	TVVTPYSAWSQBMVSLKKLLLEPNPDQFQSLSDVQNPFPYMDINWDVAFQKRLIPGFIP	300		
Qy	301	NGRGLNCDDPTFELEEMILLESKPLHKKKRLAKKEDMKKCDSSQTCLLQSHLDSVQKEFI	360		
Db	301	NGRGLNCDDPTFELEEMILLESKPLHKKKRLAKKEDMKKCDSSQTCLLQSHLDSVQKEFI	360		
Qy	361	IFNREKVNDRFNKROPNLALEQTKDPQVTNGQ	392		
Db	361	IFNREKVNDRFNKROPNLALEQTKDPQGEDGQ	392		
RESULT 8					
ID	ABU62276				
XX	ABU62276 standard; protein; 396 AA.				
AC	ABU62276;				
XX					
DT	01-SEP-2003 (first entry)				
XX					
DE	Human kinase.				
XX					
XW	Human; enzyme; kinase; gene therapy; cancer; inflammation; psoriasis;				
KW	arteriosclerosis.				
XX					
OS	Homo sapiens.				
XX					
PN	US2003027307-A1.				
XX					
PD	06-FEB-2003.				
XX					
PF	26-SEP-2002; 2002US-00254869.				
XX					
PR	09-MAR-2001; 2001US-00801876.				
XX					
PA	(APPL-) APPLERA CORP.				
XX					
PI	Ye J, Yan C, Di Francesco V, Beasley EM;				
XX					
DR	WPI; 2003-492035/58.				
DR	N-PSDB; ACA62840, ACA62841.				
XX					
PT	New isolated human kinase proteins, useful for treating disorders				
PT	mediated by kinase pathway (e.g. cancers, inflammations, arteriosclerosis				
PT	or psoriasis), or for development of human therapeutics and diagnostic				
PT	compositions.				
XX					
XX	Claim 1; Fig 2A; 185pp; English.				
XX					
CC	The invention relates to a new isolated human kinase peptide. The human				
CC	kinase peptide and nucleic acid molecules are useful in the development				
CC	of human therapeutics and diagnostic compositions. The peptides are				
CC	useful for treating disorders (e.g. cancers, inflammations,				
CC	arteriosclerosis or psoriasis) characterised by an absence of,				
CC	inappropriate, or unwanted expression of the kinase protein. These				
CC	molecules are particularly useful as models for developing human				
CC	therapeutic targets, identifying therapeutic proteins, or serving as				
CC	targets for the development of human therapeutic agents that modulate				
CC	kinase activity in cells and tissues that express the kinase. The				
CC	peptides are also useful for raising antibodies or eliciting an immune				
CC	response; as a reagent (including the labelled reagent) in assays				
CC	designed to quantitatively determine levels of the protein (or its				
CC	binding partner or ligand) in biological fluids; or as markers for				
CC	tissues in which the corresponding protein is preferentially expressed.				
CC	The agents identified are useful for treating a subject with a disorder				
CC	mediated by kinase pathway. The present sequence represents the amino				

XX The invention relates to new isolated human protein kinase polypeptide
CC and polynucleotides. The new human kinase protein is related to the
CC serine/threonine protein kinase subfamily. The kinase peptides and
CC nucleic acid molecules are useful as models for the development of human
CC therapeutic targets, aid in the identification of therapeutic proteins,
CC and serve as targets for the development of human therapeutic agents that
CC modulate kinase activity in cells and tissues that express the kinase.
CC The peptides are also useful in the diagnosis, prevention and treatment
CC of kinase-related conditions. The peptide may be used in drug screening
CC assays, in assays to determine the biological activity of the protein, to
CC raise antibodies or to elicit another immune response, as a reagent in
CC assays designed to quantitatively determine levels of the protein in
CC biological fluids, or as markers for tissues in which the corresponding
CC protein is preferentially expressed. The antibodies are useful in
CC pharmacogenomic analysis, for inhibiting protein function, or for tissue
CC typing. The nucleic acid molecules are useful as probes, primers,
CC chemical intermediates, or in biological assays. The present sequence
CC represents the amino acid sequence of the isolated human protein kinase.
XX
SQ Sequence 396 AA;

Query Match 95.2%; Score 2047; DB 8; Length 396;
Best Local Similarity 98.7%; Pred No. 7.2e-186;
Matches 387; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 MGANTSRRKPPVPDENEDVNFDFEILRAIGKSGFGKVCIVQKNDTKMYAMKMKQKCV 60
DB 1 MGANTSRRKPPVPDENEDVNFDFEILRAIGKSGFGKVCIVQKNDTKMYAMKMKQKCV 60
QY 61 ERNEVRNVFKELQIMQGLEHPELVNLWYSFQDEEDMFVVDLLGGDLRYHLQNVHFKE 120
DB 61 ERNEVRNVFKELQIMQGLEHPELVNLWYSFQDEEDMFVVDLLGGDLRYHLQNVHFKE 120
QY 121 ETVKLFICELVMDLYLQNRILHRDMKPDNILLDEHGHVHTDFNIAAMLPRETQITTM 180
DB 121 ETVKLFICELVMDLYLQNRILHRDMKPDNILLDEHGHVHTDFNIAAMLPRETQITTM 180
QY 181 ACTPYMAPEMPSSRKAGYGFVDMWSLGVTVAYELLGRPRYHRSSTSKSKEIVHFTET 240
DB 181 ACTPYMAPEMPSSRKAGYGFVDMWSLGVTVAYELLGRPRYHRSSTSKSKEIVHFTET 240
QY 241 TVVTYPSAWSQBMVSLKKLLLEPNPDQRFPSQSDVQNPYNDINWDVAFQKRLIPGPI 300
DB 241 TVVTYPSAWSQBMVSLKKLLLEPNPDQRFPSQSDVQNPYNDINWDVAFQKRLIPGPI 300
QY 301 NKGRNLNCDPTFLEEMILESPLHKKKRLAKKEDMKKCDSSOTCLLOEHLDSVQKEFI 360
DB 301 NKGRNLNCDPTFLEEMILESPLHKKKRLAKKEDMKKCDSSOTCLLOEHLDSVQKEFI 360
QY 361 IPNREKVRNDRNKPQNLALBQTKDPQVNTNGQ 392
DB 361 IPNREKVRNDRNKPQNLALBQTKDPQVNTNGQ 392

RESULT 10

ID ADF44523 standard; protein; 398 AA.
XX ADF44523;
AC ADF44523;

XX 12-FEB-2004 (first entry)

DE Mouse kinase protein SEQ ID NO:41.

KW cytosolic; nontropic; neuroprotective; antidiabetic; screening;
KW regulation; drug development; protein-associated disease; cancer;
KW dementia; diabetes; kinase; enzyme; mouse.

OS Mus musculus.

XX WO2003084992-A1.

XX

PD 16-OCT-2003.

XX 04-APR-2003; 2003WO-JP004330.

XX 05-APR-2002; 2002JP-00103396.

PR 23-APR-2002; 2002JP-00120904.

PR 02-MAY-2002; 2002JP-00130601.

XX 04-DEC-2002; 2002JP-00352520.

XX (RIKE) RIKEN KK.

PA (DNAP-) DNAPFORM KK.

PA (MITU) MITSUBISHI CHEM CORP.

XX Hayashizaki Y, Kamiya M, Kubodera H, Watanabe W;

WPI; 2003-833568/77.

DR N-FSDB; ADF44497.

XX Proteins and encoded DNAs with kinase activity, useful in screening

PT substances for regulating such activity and in developing drugs for the

PT protein-associated diseases e.g. cancer, dementia and diabetes.

XX Claim 1; SEQ ID NO 41; 342pp; Japanese.

PS The present invention describes a protein: (a) containing any of the

XX amino acid sequences of ADF44509 to ADF44534 or ADF44544; or (b) based on

CC any of the sequences in (a) but with some amino acids deleted,

CC substituted and/or added and having kinase activity. Also described: (1)

CC a DNA encoding any of the proteins; (2) a full-length cDNA encoding the

CC protein; (3) a DNA which is: (a) a DNA containing any of the base

CC sequences in ADF44483 to ADF44508 or ADF44543; (b) a DNA derived from any

CC of the sequences in (a) but with some bases deleted, substituted and/or

CC added and encoding a protein with kinase activity; or (c) a DNA

CC hybridisable with any of the sequences in (a) or their complementary

CC strands under stringent conditions and encoding a protein with kinase

CC activity; (4) a recombinant vector containing the DNA; (5) a cell

CC transfected with the DNA or recombinant vector, or an individual produced

CC from the cell; (6) recombinant proteins produced by such cells; (7) an

CC oligonucleotide containing 5-10 consecutive bases in any of the base

CC sequences, its sense oligonucleotide, an antisense oligonucleotide with a

CC complementary strand of such sense oligonucleotide, or an oligonucleotide

CC derivative of the (anti-)sense oligonucleotide; (8) an antibody

CC specifically binding to the protein, or its partial fragment; (9) a

CC method for screening substances for regulating activity of the protein by

CC contacting a test substance with such protein before measuring changes in

CC the protein activity due to the test substance; (10) a method for

CC screening substances regulating expression of the DNA by contacting a

CC test substance with cells transfected with the gene and detecting changes

CC in expression level of the DNA in such cells; (11) recordable media for

CC reading in a computer with information on the amino acid sequences of the

CC proteins, and/or base sequences of the DNAs stored; and (12) a support

CC for binding with any of the proteins and/or DNAs. The proteins and their

CC encoded DNAs have cytostatic, nontropic, neuroprotective and antidiabetic

CC activities. They can be used in screening substances for regulating such

CC activity and in developing drugs for the protein-associated diseases e.g.

CC cancer, dementia and diabetes. The present sequence is used in the

CC exemplification of the present invention.

XX SQ Sequence 398 AA;

Query Match 87.4%; Score 1880; DB 7; Length 398;
Best Local Similarity 91.2%; Pred. No. 5.8e-170;
Matches 351; Conservative 20; Mismatches 14; Indels 0; Gaps 0;

QY 1 MGANTSRRKPPVPDENEDVNFDFEILRAIGKSGFGKVCIVQKNDTKMYAMKMKQKCV 60

DB 1 MGANTSRRKPPVPDENEDVNFDFEILRAIGKSGFGKVCIVQKNDTKMYAMKMKQKCV 60

QY 61 ERNEVRNVFKELQIMQGLEHPELVNLWYSFQDEEDMFVVDLLGGDLRYHLQNVHFKE 120

DB 61 ERNEVRNVFKELQIMQGLEHPELVNLWYSFQDEEDMFVVDLLGGDLRYHLQNVHFKE 120

QY 121 ETVKLFICELVMDLYLQNRILHRDMKPDNILLDEHGHVHTDFNIAAMLPRETQITTM 180

Db 121 DTVKLFICELAMALDYLSQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPEKTRITTV 180
 Qy 181 AGTPYMAPFSSRGKAGYSAVDWWSLGVATYELLGRPPYHRSSTSSKEIVHTFET 240
 Db 181 AGTPYMAPFSSRGKAGYSAVDWWSLGVATYELLGRPPYHRSSTSSKEIVHTFET 240
 Qy 241 TVVTYPSAWSQEMVSLKLLLEPNPDORFSDVQNFPPYMDINWDVAFQKRLIPGIP 300
 Db 241 AIVTYPSAWSQEMVSLKLLLEPNPDORFSDVQNFPPYMDINWDVAFQKRLIPGIP 300
 Qy 301 NKGRINCDPTPELEEMILESPLHKKKRLAKKEMKCDSSOTCLLQHLDSVQKEFI 360
 Db 301 TKGRINCDPTPELEEMILESPLHKKKRLAKKEMKCDSSOTCLLQHLDSVQKEFI 360
 Qy 361 IFNREKVNDRPNKQPNLALEQTKD 385
 Db 361 IFNREKVSDFNQRQANLALEQTKN 385

RESULT 11

ADP44527
ID ADP44527 standard; protein; 398 AA.

XX AC ADP44527;

XX DT 12-FEB-2004 (first entry)

XX DE Mouse kinase protein SEQ ID NO:45.

XX KW cytostatic; nootropic; neuroprotective; antidiabetic; screening;
 KW regulation; drug development; protein-associated disease; cancer;
 KW dementia; diabetes; kinase; enzyme; mouse.

XX OS Mus musculus.

XX PN WO2003084992-A1.

XX PD 16-OCT-2003.

XX PF 04-APR-2003; 2003WO-JP004330.

XX PR 05-APR-2002; 2002JP-00103396.

XX PR 23-APR-2002; 2002JP-00120904.

XX PR 02-MAY-2002; 2002JP-00130601.

XX PR 04-DEC-2002; 2002JP-00325250.

XX PA (RIKE) RIKEN KK.

XX PA (DNAP-) DNAFORM KK.

XX PA (MITU) MITSUBISHI CHEM CORP.

XX PI Hayashizaki Y, Kamiya M, Kubodera H, Watanabe W;

XX DR WPI; 2003-833568/77.

XX DR N-PSDB; ADP44501.

XX PS Claim 1; SEQ ID NO 45; 342pp; Japanese.

CC The present invention describes a protein: (a) containing any of the
 CC amino acid sequences of ADP44509 to ADP44534 or ADP44544; or (b) based on
 CC any of the sequences in (a) but with some amino acids deleted.
 CC substituted and/or added and having kinase activity. Also described: (1)
 CC a DNA encoding any of the proteins; (2) a full-length cDNA encoding the
 CC protein; (3) a DNA which is: (a) a DNA containing any of the base
 CC sequences in ADP44483 to ADP44508 or ADP44543; (b) a DNA derived from any
 CC of the sequences in (a) but with some bases deleted, substituted and/or
 CC added and encoding a protein with kinase activity; or (c) a DNA
 CC hybridisable with any of the sequences in (a) or their complementary
 CC strands under stringent conditions and encoding a protein with kinase

CC activity; (4) a recombinant vector containing the DNA; (5) a cell
 CC transferred with the DNA or recombinant vector, or an individual produced
 CC from the cell; (6) recombinant proteins produced by such cells; (7) an
 CC oligonucleotide containing 5-10 consecutive bases in any of the base
 CC sequences, its sense oligonucleotide, an antisense oligonucleotide with a
 CC complementary strand of such sense oligonucleotide, or an oligonucleotide
 CC derivative of the (anti-)sense oligonucleotide; (8) an antibody
 CC specifically binding to the protein, or its partial fragment; (9) a
 CC method for screening substances for regulating activity of the protein by
 CC contacting a test substance with such protein before measuring changes in
 CC the protein activity due to the test substance; (10) a method for
 CC screening substances regulating expression of the DNA by contacting a
 CC test substance with cells transfected with the gene and detecting changes
 CC in expression level of the DNA in such cells; (11) recordable media for
 CC reading in a computer with information on the amino acid sequences of the
 CC proteins, and/or base sequences of the DNAs stored; and (12) a support
 CC for binding with any of the proteins and/or DNAs. The proteins and their
 CC encoded DNAs have cytostatic, nootropic, neuroprotective and antidiabetic
 CC activities. They can be used in screening substances for regulating such
 CC activity and in developing drugs for the protein-associated diseases e.g.
 CC cancer, dementia and diabetes. The present sequence is used in the
 CC exemplification of the present invention.

XX SQ Sequence 398 AA;

Query Match 87.2%; Score 1875; DB 7; Length 398;

Best Local Similarity 90.9%; Pred. No. 1.7e-169;

Matches 350; Conservative 21; Mismatches 14; Indels 0; Gaps 0;

Qy 1 MGANTSRKPPVFDENEDVDFEILRAIGKSGFGKVICIVQKNDTKQYAMKYNKQKCV 60

Db 1 MGANTSKAPVFDENEDVDFEILRAIGKSGFGKVICIVQKNDTKQYAMKYNKQKCV 60

Qy 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEDMFVVDLLGGDLRYHLQNVHFKE 120

Db 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEDMFVVDLLGGDLRYHLQNVHFQE 120

Qy 121 ETVKLFICELVMAIDYIQNORIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETOITTM 180

Db 121 DTVKLFICELAMALDYLSQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPEKTRITTV 180

Qy 181 AGTPYMAPFSSRGKAGYSAVDWWSLGVATYELLGRPPYHRSSTSSKEIVHTFET 240

Db 181 AGTPYMAPFSSRGKAGYSAVDWWSLGVATYELLGRPPYHRSSTSSKEIVHTFET 240

Qy 241 TVVTYPSAWSQEMVSLKLLLEPNPDORFSDVQNFPPYMDINWDVAFQKRLIPGIP 300

Db 241 AIVTYPSAWSQEMVSLKLLLEPNPDORFSDVQNFPPYMDINWDVAFQKRLIPGIP 300

Qy 301 NKGRINCDPTPELEEMILESPLHKKKRLAKKEMKCDSSOTCLLQHLDSVQKEFI 360

Db 301 TKGRINCDPTPELEEMILESPLHKKKRLAKKEMKCDSSOTCLLQHLDSVQKEFI 360

Qy 361 IFNREKVNDRPNKQPNLALEQTKD 385

Db 361 IFNREKVSDFNQRQANLALEQTKN 385

RESULT 12

ADP03989

ID ADM03989 standard; protein; 358 AA.

XX AC ADM03989;

XX DT 20-MAY-2004 (first entry)

XX DE Human protein of the invention SEQ ID NO:2674.

XX KW human; gene therapy; diagnostic marker; pharmaceutical.

XX OS Homo sapiens.

XX PN EP1347046-A1.

XX 24-SEP-2003.
PD 12-APR-2002; 2002EP-00008400.
XX PF
XX 22-MAR-2002; 2002JP-00137785.
XX PR
XX (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX WPI: 2003-7233558/69.
DR N-PSDB; ADM01546.
XX
XX New polynucleotides and polypeptides are useful in gene therapy, for
PT developing a diagnostic marker or medicines for regulating their
PT expression and activity, or as a target of gene therapy.
XX
XX Claim 1; SEQ ID NO 2674; 305pp; English.
XX
XX The invention relates to a novel human polynucleotide and the encoded
CC polypeptide. A polynucleotide of the invention may have a use in gene
CC therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful
CC as a primer for synthesizing the polynucleotide or as a probe for
CC detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are
CC useful in gene therapy, for developing a diagnostic marker or medicines
CC for regulating their expression and activity, or as a target of gene
CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides
CC are useful as pharmaceutical agents. The present sequence represents a
CC protein sequence of the invention.
XX
SQ Sequence 358 AA;

Query Match 84.9%; Score 1827; DB 7; Length 358;
Best Local Similarity 100.0%; Pred. No. 5.6e-165;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGANTSRRPPVFDENEDVNFDFEILRAIGKSGFGKVCIVQKNDTKMYAMKYNKQKCV 60
DB 1 MGANTSRRPPVFDENEDVNFDFEILRAIGKSGFGKVCIVQKNDTKMYAMKYNKQKCV 60

QY 61 ERNEVRNVFKELQIQMGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQNVHFK 120
DB 61 ERNEVRNVFKELQIQMGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQNVHFK 120

QY 121 ETVKLFICELVMDLYLQNRQRIHRDMKPDNILLDEHGHVHTDFTNIAAMLPRETQITTM 180
DB 121 ETVKLFICELVMDLYLQNRQRIHRDMKPDNILLDEHGHVHTDFTNIAAMLPRETQITTM 180

QY 181 AGTKPYMAPEMFSSRRKGAGYFAVDWWSLGVTA YELLGRPPYHRSSTSSKEIVHTPET 240
DB 181 AGTKPYMAPEMFSSRRKGAGYFAVDWWSLGVTA YELLGRPPYHRSSTSSKEIVHTPET 240

QY 241 TVVTYPSAWSQBMVSLKLLKLEPNDFQFSQSDVQNFYPMNDINWDAVFOKRLIPGIP 300
DB 241 TVVTYPSAWSQBMVSLKLLKLEPNDFQFSQSDVQNFYPMNDINWDAVFOKRLIPGIP 300

QY 301 NKGRLNCDDPTFLEEMILESPLHKKKRLAKKXDMKCDSSQ 344
DB 301 NKGRLNCDDPTFLEEMILESPLHKKKRLAKKXDMKCDSSQ 344

RESULT 13
AAU03504
ID AAU03504 standard; protein; 327 AA.
XX
XX AAU03504;
XX
XX 12-SEP-2001 (first entry)
XX
XX Human protein kinase #4.

XX Human; protein kinase; PTK; STK; cancer; cardiovascular disease;
KW metabolic disorder; immune related disease; neurological disorder;
KW neurodegenerative disorder; inflammatory disorder; infectious disease;
KW reproductive disorder.
XX Homo sapiens.
OS
XX W0200138503-A2.
FN
XX 31-MAY-2001.
PD
XX 22-NOV-2000; 2000WO-US032085.
PF
XX 24-NOV-1999; 99US-0167482P.
PR
XX (SUGB-) SUGEN INC.
PA
XX Plowman GD, Whyte D, Manning G, Sudarsanam S, Martinez R;
PI Flanagan P, Clary D;
PI
XX WPI: 2001-343950/36.
DR N-PSDB; AAS06704.
XX
XX Nucleic acids encoding human kinase polypeptides, useful for preventing
CC diagnosing and/or treating e.g. cancer, immune, cardiovascular and
CC neuronal-associated diseases, and microbial infections.
CC
CC Claim 7; Fig 2; 433pp; English.
XX
XX AAU03501-AAU03557 represent novel human protein kinases #1-57. The novel
CC protein kinases have been identified as members of the tyrosine or
CC serine/threonine kinase (PTK and STK) families. The polynucleotides
CC encoding protein kinases and the polypeptides may be used in the
CC prevention, diagnosis and treatment of diseases associated with
CC inappropriate kinase expression. For example, they may be used to treat
CC cancers (especially cancers of haematopoietic origin), cardiovascular
CC disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes),
CC immune related diseases (e.g. rheumatoid arthritis), neurological
CC disorders (e.g. schizophrenia), neurodegenerative disorders (e.g.
CC Parkinson's disease), inflammatory disorders (e.g. asthma), infectious
CC disease (e.g. HIV) and reproductive disorders (e.g. infertility).
CC Additionally, polynucleotides encoding protein kinases may be used for
CC gene therapy and as DNA probes in diagnostic assays. The protein kinase
CC polypeptides may be used as antigens in the production of antibodies
CC against the protein kinases and in assays to identify modulators of
CC protein kinase expression and activity
XX
SQ Sequence 327 AA;

Query Match 70.4%; Score 1513.5; DB 4; Length 327;
Best Local Similarity 87.6%; Pred. No. 3.5e-135;
Matches 297; Conservative 5; Mismatches 18; Indels 19; Gaps 4;

QY 1 MGANTSRRPPVFDENEDVNFDFEILRAIGKSGFGKVCIVQKNDTKMYAMKYNKQKCV 60
DB 1 MGANTSRRPPVFDENEDVNFDFEILRAIGKSGFGKVCIVQKNDTKMYAMKYNKQKCV 60

QY 61 ERNEVRNVFKELQIQMGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQNVHFK 120
DB 61 ERNEVRNVFKELQIQMGLEHPFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQNVHFK 120

QY 121 ETVKLFICELVMDLYLQNRQRIHRDMKPDNILLDEHGHVHTDFTNIAAMLPRETQITTM 180
DB 121 ETVKLFICELVMDLYLQNRQRIHRDMKPDNILLDEHGHVHTDFTNIAAMLPRETQITTM 180

QY 181 AGTKPYMAPEMFSSRRKGAGYFAVDWWSLGVTA YELLGRPPYHRSSTSSKEIVHTPET 240
DB 181 AGTKPYMAPEMFSSRRKGAGYFAVDWWSLGVTA YELLGRPPYHRSSTSSKEIVHTPET 240

QY 241 TVVTYPSAWSQBMVSLKLLKLEPNDFQFSQSDVQNFYPMNDINWDAVFOKRLIPGIP 300
DB 241 TVVTYPSAWSQBMVSLKLLKLEPNDFQFSQSDVQNFYPMNDINWDAVFOKRLIPGIP 300

QY 301 NKGRLNCDDPTFLEEMILESPLHKKKRLAKKXDMKCDSSQ 344
DB 301 NKGRLNCDDPTFLEEMILESPLHKKKRLAKKXDMKCDSSQ 344

RESULT 13
AAU03504
ID AAU03504 standard; protein; 327 AA.
XX
XX AAU03504;
XX
XX 12-SEP-2001 (first entry)
XX
XX Human protein kinase #4.

CC pharmacogenomic analysis, for inhibiting protein function, or for tissue
CC typing. The nucleic acid molecules are useful as probes, primers,
CC chemical intermediates, or in biological assays. The present sequence
CC represents the amino acid sequence of a serine/threonine protein kinase
CC used in homology comparison of the new isolated human protein kinase.
XX
XX

SQ Sequence 404 AA;

```
Query Match          66.5%; Score 1430.5; DB 8; Length 404;
Best Local Similarity 68.1%; Pred. No. 3.8e-127;
Matches 280; Conservative 43; Mismatches 71; Indels 17; Gaps 5;

QY 1 MGNATSRKPPVDEEDVNFHFEILRAIGKSGFKVCIVQKNDTKKMYAMKMKQCV 60
Db 1 MGNHSHKPPVDEEDVNFHFEILRAIGKSGFKVCIVQKNDTKKMYAMKMKQCV 60

QY 61 -ERNEVRNVFKELQIMQGLEHPLVNLWYSFODEEDMFVVDLLGGDLRYHLQONVHF 119
Db 61 QERDEVNRVFRLEQIMQGLEHPLVNLWYSFODEEDMFVVDLLGGDLRYHLQONVHT 120

QY 120 EETVKLFICELVMDLYLQNRHIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETOITT 179
Db 121 EGTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEHGHVHITDFNIAATVLKSEKASS 180

QY 180 MAGTKPYNAPEMPS--SRKGAGYSPADVWWSLGVATAYELLGRRPYHRSSTSSKEIVHT 237
Db 181 MAGTKPYNAPEYFQYVVDGGGCGSYVDVWSLGVATAYELLGRWRPYEIHSAITPIDEILNM 240

QY 238 FETTVTVYPSAWSQEMVSLKKLEPNPDQPSQLSDYQNFPMNDINWDADVFOKRLPG 297
Db 241 FKVERVHYSSTWCEGNVSLKKLLTKDPESRLSSLRDIQSWTYLADMWDADVFEKALMPG 300

QY 298 FIPNKGRLNCDPTPELEEMILESPLHKKKKRLAK-KEKDMRKCDSSQTCLLQSHLDSVQ 356
Db 301 FVPNKGRLNCDPTPELEEMILESPLHKKKKRLAKHRSRSDTKDSCPLNGHLQQCLETVR 360

QY 357 KEFIIFNREKVNDFNKPQNLALQTKDPQVT--NGQMDTGLSETFTQTSK 405
Db 361 KEFIIFNREKLRR-----QQGHGQQLDLGRIQSQTSSKLQDGR 400
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Search completed: December 17, 2004, 09:28:01
Job time : 75 secs

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OM protein - protein search, using sw model

Run on: December 17, 2004, 09:25:19 ; Search time 21 Seconds
(without alignments)
1285.306 Million cell updates/sec

Title: US-10-620-845-9

Perfect score: 2151

Sequence: 1 MGANTSRRKPPVFEDNEVDNF.....VTNGQMDTGLSEFTQTSKVS 407

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

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- 2: /cgn2_6/ptodata/1/iaa/5B COMB.pap.*
- 3: /cgn2_6/ptodata/1/iaa/6A COMB.pap.*
- 4: /cgn2_6/ptodata/1/iaa/6B COMB.pap.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pap.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2151	100.0	407	4	US-09-841-683-9
2	2060	95.8	396	4	US-09-841-683-11
3	2047	95.2	396	4	US-09-801-876B-2
4	2047	95.2	396	4	US-10-254-869-2
5	1430.5	66.5	404	4	US-09-801-876B-4
6	1430.5	66.5	404	4	US-10-254-869-4
7	1423.5	66.2	403	4	US-09-801-876B-5
8	1423.5	66.2	403	4	US-10-254-869-5
9	1332.5	61.9	419	4	US-09-799-875-14
10	1328.5	61.8	384	4	US-09-801-876B-6
11	1328.5	61.8	384	4	US-10-254-869-6
12	1294.5	60.2	399	4	US-09-819-607-4
13	1174	54.6	236	4	US-09-841-683-7
14	1174	54.4	225	4	US-09-841-683-5
15	1142	53.1	369	4	US-09-819-607-2
16	1127.5	52.4	368	4	US-09-819-607-5
17	995.5	46.3	316	4	US-09-801-876B-7
18	995.5	46.3	316	4	US-10-254-869-7
19	852.5	39.6	347	4	US-09-801-876B-8
20	852.5	39.6	347	4	US-10-254-869-8
21	525	23.4	470	4	US-09-248-796A-18482
22	514.5	23.9	740	4	US-09-538-092-1178
23	509.5	23.7	336	4	US-09-394-455-2
24	509.5	23.7	343	4	US-09-394-455-15
25	509.5	23.7	343	4	US-09-394-455-34
26	509.5	23.7	350	4	US-09-538-092-946
27	509.5	23.7	351	4	US-09-394-455-4

28	508.5	23.6	587	1	US-08-313-274-2	Sequence 2, Appli
29	504.5	23.5	398	4	US-09-538-092-501	Sequence 501, App
30	503.5	23.4	343	4	US-09-394-455-38	Sequence 38, Appl
31	503.5	23.4	350	3	US-09-457-040B-37	Sequence 37, Appli
32	503.5	23.4	351	3	US-09-457-040B-6	Sequence 6, Appli
33	503.5	23.4	595	4	US-09-417-197-69	Sequence 69, Appli
34	498.5	23.2	689	1	US-08-221-817-18	Sequence 18, Appli
35	498.5	23.2	689	1	US-08-454-439-18	Sequence 18, Appli
36	498.5	23.2	689	5	PCT-US94-10487-18	Sequence 18, Appli
37	497.5	23.1	350	4	US-09-538-092-991	Sequence 991, App
38	495.5	23.0	481	4	US-09-538-092-1054	Sequence 1054, Ap
39	485.5	22.6	699	1	US-08-221-817-20	Sequence 20, Appli
40	485.5	22.6	699	1	US-08-454-439-20	Sequence 20, Appli
41	485.5	22.6	699	5	PCT-US94-10487-20	Sequence 20, Appli
42	485	22.5	260	2	US-07-857-224B-8	Sequence 8, Appli
43	484	22.5	260	2	US-07-857-224B-7	Sequence 7, Appli
44	484	22.5	403	4	US-09-248-796A-20519	Sequence 20519, A
45	483	22.5	480	4	US-09-590-740-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1

US-09-841-683-9

; Sequence 9, Application US/09841683

; Patent No. 6617147

; GENERAL INFORMATION:

; APPLICANT: Hu, Yi

; APPLICANT: Nepomnichy, Boris

; APPLICANT: Wang, Xiaoming

; APPLICANT: Donoho, Gregory

; APPLICANT: Scoville, John

; APPLICANT: Walke, D. Wade

; TITLE OF INVENTION: No. 6617147el Human Kinase Proteins and Polynucleotides Encoding

; FILE REFERENCE: LEX-0167-USA

; CURRENT APPLICATION NUMBER: US/09/841,683

; PRIOR FILING DATE: 2001-04-24

; PRIOR APPLICATION NUMBER: US 60/199,499

; PRIOR FILING DATE: 2000-04-25

; PRIOR APPLICATION NUMBER: US 60/201,227

; PRIOR FILING DATE: 2000-05-01

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 9

; LENGTH: 407

; TYPE: PRT

; ORGANISM: homo sapiens

US-09-841-683-9

Query Match 100.0%; Score 2151; DB 4; Length 407;

Best Local Similarity 100.0%; Pred. No. 1.7e-197;

Matches 407; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MGANTSRRKPPVFEDNEVDNFHEILRAIGKSGFKVCIVQKNDTKMYAMKYNKQKV	60
Db	1	MGANTSRRKPPVFEDNEVDNFHEILRAIGKSGFKVCIVQKNDTKMYAMKYNKQKV	60
Qy	61	ERNEVRNVFKELOIMQGLEHPFLVNLWYSFQDEDMFVVDLLGGDLRYHLQNVHPKE	120
Db	61	ERNEVRNVFKELOIMQGLEHPFLVNLWYSFQDEDMFVVDLLGGDLRYHLQNVHPKE	120
Qy	121	ETVKLFCELVMDYLNQRIIHRDMKPNILLDEHGHVHITDFNIAAMLPRETQITTM	180
Db	121	ETVKLFCELVMDYLNQRIIHRDMKPNILLDEHGHVHITDFNIAAMLPRETQITTM	180
Qy	181	AGTKPYMAPFSSRRKAGYSFVDMWSLGVATYELLGRRPYHIRSTSSKEIVHPTET	240
Db	181	AGTKPYMAPFSSRRKAGYSFVDMWSLGVATYELLGRRPYHIRSTSSKEIVHPTET	240
Qy	241	TVVTYPSAWSOEVMYSLKLLPEPNDFQSFQSDVQNFPPYMNNDINWDAVFQKRLIPGIP	300
Db	241	TVVTYPSAWSOEVMYSLKLLPEPNDFQSFQSDVQNFPPYMNNDINWDAVFQKRLIPGIP	300

QY 301 NKGRNCPTPELEEMILESPLHKKKKRLAKKEDMRKCDSSQTCCLQEHLDVSQKEFI 360
Db 301 NKGRNCPTPELEEMILESPLHKKKKRLAKKEDMRKCDSSQTCCLQEHLDVSQKEFI 360
QY 361 IFNREKVNDRFNKQPNLALQEQTKDPQVINGQMDTGLSETFQTSKVS 407
Db 361 IFNREKVNDRFNKQPNLALQEQTKDPQVINGQMDTGLSETFQTSKVS 407

RESULT 2

US-09-841-683-11
; Sequence 11, Application US/09841683
; Patent No. 6617147
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Nepomnichy, Boris
; APPLICANT: Wang, Xiaoming
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Walke, D. Wade
; FILE REFERENCE: No. 6617147el Human Kinase Proteins and Polynucleotides Encoding
; TITLE OF INVENTION: LEX-0167-USA
; CURRENT APPLICATION NUMBER: US/09/841,683
; CURRENT FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: US 60/199,499
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US 60/201,227
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-841-683-11

Query Match 95.8%; Score 2060; DB 4; Length 396;
Best Local Similarity 99.2%; Pred. No. 8.5e-189;
Matches 389; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGANTSRRKPPVFDENEDVNFDFHETLRAIGKSGFKVCIVQKNDTKKQYAMKYNKQKCV 60
Db 1 MGANTSRRKPPVFDENEDVNFDFHETLRAIGKSGFKVCIVQKNDTKKQYAMKYNKQKCV 60
QY 61 ERNEVRNVFKELQIMQGLEHPEFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120
Db 61 ERNEVRNVFKELQIMQGLEHPEFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120
QY 121 ETVKLFICELVMDLYLQNRRIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTM 180
Db 121 ETVKLFICELVMDLYLQNRRIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTM 180
QY 181 AGTKPYMAPENFSSRKAGYSFVDWWSLGVTAVELLRGRPHYRSTSSKEIVHTFET 240
Db 181 AGTKPYMAPENFSSRKAGYSFVDWWSLGVTAVELLRGRPHYRSTSSKEIVHTFET 240
QY 241 TVVTYPSAWSQEMVSLKLLKLEPNPDRFSQSDVQNFPPYMDINWDVAFQKRLIPGFIP 300
Db 241 TVVTYPSAWSQEMVSLKLLKLEPNPDRFSQSDVQNFPPYMDINWDVAFQKRLIPGFIP 300
QY 301 NKGRNCPTPELEEMILESPLHKKKKRLAKKEDMRKCDSSQTCCLQEHLDVSQKEFI 360
Db 301 NKGRNCPTPELEEMILESPLHKKKKRLAKKEDMRKCDSSQTCCLQEHLDVSQKEFI 360
QY 361 IFNREKVNDRFNKQPNLALQEQTKDPQVINGQ 392
Db 361 IFNREKVNDRFNKQPNLALQEQTKDPQGEDQ 392

RESULT 3

US-09-801-876B-2
; Sequence 2, Application US/09801876B

; Patent No. 6492155
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001160
; CURRENT APPLICATION NUMBER: US/09/801,876B
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Human
US-09-801-876B-2

Query Match 95.2%; Score 2047; DB 4; Length 396;
Best Local Similarity 98.7%; Pred. No. 1.5e-187;
Matches 387; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGANTSRRKPPVFDENEDVNFDFHETLRAIGKSGFKVCIVQKNDTKKQYAMKYNKQKCV 60
Db 1 MGANTSRRKPPVFDENEDVNFDFHETLRAIGKSGFKVCIVQKNDTKKQYAMKYNKQKCV 60
QY 61 ERNEVRNVFKELQIMQGLEHPEFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120
Db 61 ERNEVRNVFKELQIMQGLEHPEFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120
QY 121 ETVKLFICELVMDLYLQNRRIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTM 180
Db 121 ETVKLFICELVMDLYLQNRRIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTM 180
QY 181 AGTKPYMAPENFSSRKAGYSFVDWWSLGVTAVELLRGRPHYRSTSSKEIVHTFET 240
Db 181 AGTKPYMAPENFSSRKAGYSFVDWWSLGVTAVELLRGRPHYRSTSSKEIVHTFET 240
QY 241 TVVTYPSAWSQEMVSLKLLKLEPNPDRFSQSDVQNFPPYMDINWDVAFQKRLIPGFIP 300
Db 241 TVVTYPSAWSQEMVSLKLLKLEPNPDRFSQSDVQNFPPYMDINWDVAFQKRLIPGFIP 300
QY 301 NKGRNCPTPELEEMILESPLHKKKKRLAKKEDMRKCDSSQTCCLQEHLDVSQKEFI 360
Db 301 NKGRNCPTPELEEMILESPLHKKKKRLAKKEDMRKCDSSQTCCLQEHLDVSQKEFI 360
QY 361 IFNREKVNDRFNKQPNLALQEQTKDPQVINGQ 392
Db 361 IFNREKVNDRFNKQPNLALQEQTKDPQGEDQ 392

RESULT 4

US-10-254-869-2
; Sequence 2, Application US/10254869
; Patent No. 6653117

; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001160DIV
; CURRENT APPLICATION NUMBER: US/10/254,869
; CURRENT FILING DATE: 2002-09-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Human
US-10-254-869-2

Query Match 95.2%; Score 2047; DB 4; Length 396;
Best Local Similarity 98.7%; Pred. No. 1.5e-187;
Matches 387; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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Qy 1 MGANTSRRPPVFDENEDVDFHFEILRAIGKSGFGKVCIVQKNDTKKMYAMKYNKQCV 60
Db 1 MGANTSRRPPVFDENEDVDFHFEILRAIGKSGFGKVCIVQKNDTKKMYAMKYNKQCV 60
Qy 61 ERNEVRNVFKELQIMOGLEHPFLVNLWYSFQDEEDFMVVDLLGGDLRYHLQONVHFK 120
Db 61 ERNEVRNVFKELQIMOGLEHPFLVNLWYSFQDEEDFMVVDLLGGDLRYHLQONVHFK 120
Qy 121 ETVKLFICELVMDALYQNRQIIRDMKPNILLDEGHVHITDFNIAAMLPRETOITTT 180
Db 121 ETVKLFICELVMDALYQNRQIIRDMKPNILLDEGHVHITDFNIAAMLPRETOITTT 180
Qy 181 AGTKPYMAPFSSRRKAGYSFAVDWMSLGVATAYELLGRPRPYHRSSTSSKEIVHTFET 240
Db 181 AGTKPYMAPFSSRRKAGYSFAVDWMSLGVATAYELLGRPRPYHRSSTSSKEIVHTFET 240
Qy 241 TVVTYPSAWSQEWVSLKLLKLEPNPDQFQSDVQNPFPYMDINWDVAFQKRLIPGIP 300
Db 241 TVVTYPSAWSQEWVSLKLLKLEPNPDQFQSDVQNPFPYMDINWDVAFQKRLIPGIP 300
Qy 301 NKGRINCDPTFELEEMILESKPLHKKKRLAK-KEKDMRKCDSSOTCLLQHLDSVQKEFI 360
Db 301 NKGRINCDPTFELEEMILESKPLHKKKRLAK-KEKDMRKCDSSOTCLLQHLDSVQKEFI 360
Qy 361 IFNREKVNDRDNKQPNLALQTKDPQVNTGQ 392
Db 361 IFNREKVNDRDNKQPNLALQTKDPQGEDGQ 392
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RESULT 5
US-09-801-876B-4
; Sequence 4, Application US/09801876B
; Patent No. 6492155
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001160
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Mus Musculus
US-09-801-876B-4
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Query Match 66.5%; Score 1430.5; DB 4; Length 404;
Best Local Similarity 68.1%; Pred. No. 1.6e-128;
Matches 280; Conservative 43; Mismatches 71; Indels 17; Gaps 5;

Qy 1 MGANTSRRPPVFDENEDVDFHFEILRAIGKSGFGKVCIVQKNDTKKMYAMKYNKQCV 60
Db 1 MGNHSHKPPVFDENEERVDHFQILRAIGKSGFGKVCIVQKRTKKMYAMKYNKQCV 60
Qy 61 -ERNEVRNVFKELQIMOGLEHPFLVNLWYSFQDEEDFMVVDLLGGDLRYHLQONVHFK 119
Db 61 QERDEVNVRVRELQIMOGLEHPFLVNLWYSFQDEEDFMVVDLLGGDLRYHLQONVHT 120
Qy 120 EETVKLFICELVMDALYQNRQIIRDMKPNILLDEGHVHITDFNIAAMLPRETOITT 179
Db 121 EGTVKLYICELALALEYLQRYHIIHRDKPNILLDEGHVHITDFNIAATVLKSEKASS 180
Qy 180 MAGTKPYMAPFMS--SRKAGYSFAVDWMSLGVATAYELLGRPRPYHRSSTSSKEIVHT 237
Db 181 MAGTKPYMAPFVQVYDGGPGYSYPVDMWSLGVATAYELLGRWPYHRSATPIDEILNM 240
Qy 238 FETTVVTPSAWSQEWVSLKLLKLEPNPDQFQSDVQNPFPYMDINWDVAFQKRLIPG 297
Db 241 FKVERVHYSTWCEGMVSLKLLKLTQDPESRLSLRDIQSMTYLADNWDVAFKALMPG 300
Qy 298 FPNKGRINCDPTFELEEMILESKPLHKKKRLAK-KEKDMRKCDSSOTCLLQHLDSVQ 356
Db 301 FVFNKGRINCDPTFELEEMILESKPLHKKKRLAKHRSRSTKDCSCLNGHLQOCLEIVR 360
Qy 357 KEFTIIFNREKVNDRDNKQPNLALQTKDPQVNTGQ 405
Db 361 KEFTIIFNREKLR-----QQGHGQSLDLDGRIGSQTSSKLDQGR 400
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RESULT 7
US-09-801-876B-5
; Sequence 5, Application US/09801876B
; Patent No. 6492155
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001160
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Qy 298 FPNKGRINCDPTFELEEMILESKPLHKKKRLAK-KEKDMRKCDSSOTCLLQHLDSVQ 356
Db 301 FVFNKGRINCDPTFELEEMILESKPLHKKKRLAKHRSRSTKDCSCLNGHLQOCLEIVR 360
Qy 357 KEFTIIFNREKVNDRDNKQPNLALQTKDPQVNTGQ 405
Db 361 KEFTIIFNREKLR-----QQGHGQSLDLDGRIGSQTSSKLDQGR 400

RESULT 6
US-10-254-869-4
; Sequence 4, Application US/10254869
; Patent No. 6653117
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001160DIV
; CURRENT APPLICATION NUMBER: US/10/254,869
; CURRENT FILING DATE: 2002-09-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Mus Musculus
US-10-254-869-4
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Query Match 66.5%; Score 1430.5; DB 4; Length 404;
Best Local Similarity 68.1%; Pred. No. 1.6e-128;
Matches 280; Conservative 43; Mismatches 71; Indels 17; Gaps 5;

Qy 1 MGANTSRRPPVFDENEDVDFHFEILRAIGKSGFGKVCIVQKNDTKKMYAMKYNKQCV 60
Db 1 MGNHSHKPPVFDENEERVDHFQILRAIGKSGFGKVCIVQKRTKKMYAMKYNKQCV 60
Qy 61 -ERNEVRNVFKELQIMOGLEHPFLVNLWYSFQDEEDFMVVDLLGGDLRYHLQONVHFK 119
Db 61 QERDEVNVRVRELQIMOGLEHPFLVNLWYSFQDEEDFMVVDLLGGDLRYHLQONVHT 120
Qy 120 EETVKLFICELVMDALYQNRQIIRDMKPNILLDEGHVHITDFNIAAMLPRETOITT 179
Db 121 EGTVKLYICELALALEYLQRYHIIHRDKPNILLDEGHVHITDFNIAATVLKSEKASS 180
Qy 180 MAGTKPYMAPFMS--SRKAGYSFAVDWMSLGVATAYELLGRPRPYHRSSTSSKEIVHT 237
Db 181 MAGTKPYMAPFVQVYDGGPGYSYPVDMWSLGVATAYELLGRWPYHRSATPIDEILNM 240
Qy 238 FETTVVTPSAWSQEWVSLKLLKLEPNPDQFQSDVQNPFPYMDINWDVAFQKRLIPG 297
Db 241 FKVERVHYSTWCEGMVSLKLLKLTQDPESRLSLRDIQSMTYLADNWDVAFKALMPG 300
Qy 298 FPNKGRINCDPTFELEEMILESKPLHKKKRLAK-KEKDMRKCDSSOTCLLQHLDSVQ 356
Db 301 FVFNKGRINCDPTFELEEMILESKPLHKKKRLAKHRSRSTKDCSCLNGHLQOCLEIVR 360
Qy 357 KEFTIIFNREKVNDRDNKQPNLALQTKDPQVNTGQ 405
Db 361 KEFTIIFNREKLR-----QQGHGQSLDLDGRIGSQTSSKLDQGR 400
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RESULT 7
US-09-801-876B-5
; Sequence 5, Application US/09801876B
; Patent No. 6492155
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001160
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; CURRENT APPLICATION NUMBER: US/09/801.876B
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Human
US-09-801-876B-5

Query Match 66.2%; Score 1423.5; DB 4; Length 403;
Best Local Similarity 72.3%; Pred. No. 7.4e-128;
Matches 269; Conservative 40; Mismatches 60; Indels 3; Gaps 2;

QY 1 MGNTSRKPPVFDENEDVNFDFEILRAIGKSGFGKVCIVQKNDTKMYAMKYNKQKCV 60
DB 1 MGNHSHKPPVFDENEENVFDFHQLRAIGKSGFGKVCIVQKNDTKMYAMKYNKQKCI 60
QY 61 ERNEVRNVFKELQIMQGLEHFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFK 120
DB 61 ERDEVRNVFRELQIMQGLEHFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFT 120
QY 121 ETVKLFICELVMDALYQNRQIHRDKMKNLILDEHGHVHITDFNTAAMLPRQTQITM 180
DB 121 GTVKLYICELALALEYLQRYHIHRDIKPDNILLDEHGHVHITDFNATVVKGAERASSM 180
QY 181 AGTKPYMAPEMFS--SRKAGYSFADVWMSLGVTAYELLRGRRPYHRSSTSSKEIVHTF 238
DB 181 AGTKPYMAPEVQVYMDRPGYSVPDWSLIGITAYELLRGRWRPYEHSVTPIDEILNMF 240
QY 239 ETTVVTPYSAWSQEMVSLKLLLEPNPDQSFQSDVQNFYMDINWDVAFQKRLIPGF 298
DB 241 KVERVHYSSTWCKGMVALLRKLTKDPESVSSLHDIQSVPYLADMNDVAFKKALMPGF 300
QY 299 IPNKGRLNCDPTFELEEMILESPLHKKKKLAK-KEKDMRKCDSSTCLLQEHLDVQK 357
DB 301 VPNGRLNCDPTFELEEMILESPLHKKKKLAKNRSDGTGKSCPLNGHLQCHLETVRE 360
QY 358 EPIIFNREKVR 369
DB 361 EPIIFNREKLRR 372

RESULT 8
US-10-254-869-5
; Sequence 5, Application US/10254869
; Patent No. 653117
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001160DIV
; CURRENT APPLICATION NUMBER: US/10/254.869
; CURRENT FILING DATE: 2002-09-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Human
US-10-254-869-5

Query Match 66.2%; Score 1423.5; DB 4; Length 403;
Best Local Similarity 72.3%; Pred. No. 7.4e-128;
Matches 269; Conservative 40; Mismatches 60; Indels 3; Gaps 2;

QY 1 MGNTSRKPPVFDENEDVNFDFEILRAIGKSGFGKVCIVQKNDTKMYAMKYNKQKCV 60
DB 1 MGNHSHKPPVFDENEENVFDFHQLRAIGKSGFGKVCIVQKNDTKMYAMKYNKQKCI 60
QY 61 ERNEVRNVFKELQIMQGLEHFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFK 120
DB 61 ERDEVRNVFRELQIMQGLEHFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFT 120

DB 61 ERDEVRNVFRELQIMQGLEHFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFT 120
QY 121 ETVKLFICELVMDALYQNRQIHRDKMKNLILDEHGHVHITDFNTAAMLPRQTQITM 180
DB 121 GTVKLYICELALALEYLQRYHIHRDIKPDNILLDEHGHVHITDFNATVVKGAERASSM 180
QY 181 AGTKPYMAPEMFS--SRKAGYSFADVWMSLGVTAYELLRGRRPYHRSSTSSKEIVHTF 238
DB 181 AGTKPYMAPEVQVYMDRPGYSVPDWSLIGITAYELLRGRWRPYEHSVTPIDEILNMF 240
QY 239 ETTVVTPYSAWSQEMVSLKLLLEPNPDQSFQSDVQNFYMDINWDVAFQKRLIPGF 298
DB 241 KVERVHYSSTWCKGMVALLRKLTKDPESVSSLHDIQSVPYLADMNDVAFKKALMPGF 300
QY 299 IPNKGRLNCDPTFELEEMILESPLHKKKKLAK-KEKDMRKCDSSTCLLQEHLDVQK 357
DB 301 VPNGRLNCDPTFELEEMILESPLHKKKKLAKNRSDGTGKSCPLNGHLQCHLETVRE 360
QY 358 EPIIFNREKVR 369
DB 361 EPIIFNREKLRR 372

RESULT 9
US-09-799-875-14
; Sequence 14, Application US/09799875
; Patent No. 6638721
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Williamson, Mark
; TITLE OF INVENTION: No. 6638721el Human Protein Kinases and Uses
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: 35800/209996
; CURRENT APPLICATION NUMBER: US/09/799.875
; CURRENT FILING DATE: 2001-03-06
; PRIOR FILING DATE: 2000-02-11
; PRIOR FILING DATE: 2000-02-11
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-799-875-14

Query Match 61.9%; Score 1332.5; DB 4; Length 419;
Best Local Similarity 65.0%; Pred. No. 4e-119;
Matches 253; Conservative 55; Mismatches 76; Indels 5; Gaps 3;

QY 1 MGNTSRKPPVFDENEDVNFDFEILRAIGKSGFGKVCIVQKNDTKMYAMKYNKQKCV 60
DB 5 MSAATARR--PVFDDKEDVNFDFHQLRAIGKSGFGKVCIVQKNDTKMYAMKYNKQKCI 63
QY 61 ERNEVRNVFKELQIMQGLEHFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFK 120
DB 64 ERDEVRNVFRELQIMQGLEHFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFT 123
QY 121 ETVKLFICELVMDALYQNRQIHRDKMKNLILDEHGHVHITDFNTAAMLPRQTQITM 180
DB 124 DTVELYICEMALADLYLRGQHIHRDVKPDNILLDERGHAHLTDFNTATIKDGERATAL 183
QY 181 AGTKPYMAPEMFS--RKGAGYSFADVWMSLGVTAYELLRGRRPYHRSSTSSKEIVHTF 238
DB 184 AGTKPYMAPEIFHSFVNGGTGYSFVDMVSWGVWYELLRGRPYDTHSSNAVESLQOLF 243
QY 239 ETTVVTPYSAWSQEMVSLKLLLEPNPDQSFQSDVQNFYMDINWDVAFQKRLIPGF 298
DB 244 STVSQVQVPTFSKEMVALLRKLTVNPEHRLSSIQDVQAAPALAGVLMDHLSEKRVPGF 303
QY 299 IPNKGRLNCDPTFELEEMILESPLHKKKKLAKKEKDMRKCDSST--CLLQEHLDVQK 356

	Query March	60.2%;	Score 1294.5;	DB 4;	Length 399;	
	Best Local Similarity	63.4%;	Pred. No. 1.6e-115;			
	Matches 248;	Conservative 54;	Mismatches 80;	Indels 9;	Gaps 3;	
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Dd	:	1	VNPDHFLRAIGKSGFKYCIIVKRDTEKMYAMKYNNKCQIERDEVNRVFRLEILQE	60		
Qy	:	78	LEHDPLNLNLYSFODEDMFMVDLLGGDLRYHLQQNVHPKETVKLFICELYNMADYL	137		
Dd	:	61	IEHFVLNLNLYSFODEDMFMVDLLGGDLRYHLQQNVQSEDTVRUYICEMLAUDYL	120		


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Db      1 MYANKYKQOCIERDEVNFRLEILQIEHVFNLNYSFQDEBDMFVVDLLGSD 60
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Db      61 LRYHLQNVQFSEDTVALYICEMALADYLRGQHIHRDVKPDNILLDERGHAHLTDFNI 120
Qy      168 AAMLPRETOITTMAGTKPYMAPENFSS--RKGAGYSFVAVDWSLGVTAAYELLRGRRPYHI 225
Db      121 ATIIKDGERTALAGTRPYMAPEIFHSFVNGGTGYSFVDMWSVGVMAAYELLRGWRPYDI 180
Qy      226 RSSTSKEIVHTFETTVVTPSAWSQEMVSLKLLPENPDORFSQLSDVQNFPPYMDIN 285
Db      181 HSSNAVSLSVQLFSTVSQYVPTWSKEMVALLRKLTVNPEHRLSSLDVQAAAPALAGVL 240
Qy      286 WDAVFQKRLIPGFIPNKGRLNCDPTFELEEMILES KPLHKKKKRLAKKEDMRKCDSSQT 345
Db      241 WDHLSEKRVGFGVFNKGRHLHCDPTFELEEMILES RPLHKKKKRLAKKSRDNRDSSQS 300
Qy      346 --CLLQEHLSVQKEFIIFNREKVNDRDNKQPNLALEQTKD 385
Db      301 ENDYLODCLDAIQODFVFNREKLKRSQDLPREPLPAPESRD 342
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Search completed: December 17, 2004, 09:29:11
Job time : 23 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 17, 2004, 09:28:08 ; Search time 946 Seconds
(without alignments)
153.952 Million cell updates/sec

Title: US-10-620-845-9

Perfect score: 2151

Sequence: 1 MGANTSRRPPVDFENEDVNF.....VTNGQMDTGLSETFTSKVS 407

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1589859 seqs, 357834939 residues

Total number of hits satisfying chosen parameters: 1589859

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2151	100.0	407	9	US-09-841-683-9
2	2151	100.0	407	16	US-10-620-845-9
3	2060	95.8	396	9	US-09-841-683-11
4	2060	95.8	396	14	US-10-288-798-20
5	2060	95.8	396	15	US-10-362-892-20
6	2060	95.8	396	15	US-10-182-243-33
7	2060	95.8	396	15	US-10-620-845-11
8	2054	95.5	396	15	US-10-410-764-101
9	2047	95.2	396	9	US-09-801-876B-2
10	2047	95.2	396	14	US-10-254-869-2
11	2047	95.2	396	15	US-10-667-442-2
12	1827	84.9	358	15	US-10-108-260A-2674
13	1441	67.0	414	15	US-10-074-978A-158

14	1430.5	66.5	404	9	US-09-801-876B-4	Sequence 4, Appli
15	1430.5	66.5	404	14	US-10-254-869-4	Sequence 4, Appli
16	1430.5	66.5	404	15	US-10-667-442-4	Sequence 4, Appli
17	1423.5	66.2	403	9	US-09-801-876B-5	Sequence 5, Appli
18	1423.5	66.2	403	14	US-10-254-869-5	Sequence 5, Appli
19	1423.5	66.2	403	15	US-10-667-442-5	Sequence 5, Appli
20	1423.5	66.2	403	15	US-10-354-358-36	Sequence 36, Appli
21	1423.5	66.2	414	14	US-10-074-978A-157	Sequence 157, App
22	1423.5	66.2	414	15	US-10-074-978A-154	Sequence 154, App
23	1332.5	61.9	419	9	US-09-799-875-14	Sequence 14, Appli
24	1332.5	61.9	419	14	US-10-303-664A-6	Sequence 6, Appli
25	1332.5	61.9	419	15	US-10-649-156-14	Sequence 14, Appli
26	1332.5	61.9	485	17	US-10-618-941-75	Sequence 75, Appli
27	1331	61.9	485	15	US-10-415-011-12	Sequence 12, Appli
28	1328.5	61.8	384	9	US-09-801-876B-6	Sequence 6, Appli
29	1328.5	61.8	384	14	US-10-254-869-6	Sequence 6, Appli
30	1328.5	61.8	384	15	US-10-667-442-6	Sequence 18, Appli
31	1310.5	60.9	488	15	US-10-074-978A-18	Sequence 4, Appli
32	1294.5	60.2	399	10	US-09-819-607-4	Sequence 4, Appli
33	1294.5	60.2	399	15	US-10-633-631-4	Sequence 4, Appli
34	1272.5	59.2	375	15	US-10-168-582-12	Sequence 12, Appli
35	1186.5	55.2	364	13	US-10-052-586-572	Sequence 572, App
36	1186.5	55.2	364	14	US-10-174-590-572	Sequence 572, App
37	1186.5	55.2	364	14	US-10-176-758-572	Sequence 572, App
38	1186.5	55.2	364	14	US-10-175-737-572	Sequence 572, App
39	1186.5	55.2	364	14	US-10-174-581-572	Sequence 572, App
40	1186.5	55.2	364	14	US-10-176-483-572	Sequence 572, App
41	1186.5	55.2	364	14	US-10-176-749-572	Sequence 572, App
42	1186.5	55.2	364	14	US-10-176-914-572	Sequence 572, App
43	1186.5	55.2	364	14	US-10-176-915-572	Sequence 572, App
44	1186.5	55.2	364	14	US-10-173-706-572	Sequence 572, App
45	1186.5	55.2	364	14	US-10-175-738-572	Sequence 572, App

ALIGNMENTS

RESULT 1

US-09-841-683-9
; Sequence 9, Application US/09841683
; Patent No. US20020081600A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Nepomnichy, Boris
; APPLICANT: Wang, Xiaoming
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Walke, D. Wade
; TITLE OF INVENTION: No. US20020081600A1el Human Kinase Proteins and Polynucleotides E
; FILE REFERENCE: LEX-0167-USA
; CURRENT APPLICATION NUMBER: US/09/841,683
; CURRENT FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: US 60/199,499
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US 60/201,227
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 407
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-841-683-9

Query Match 100.0%; Score 2151; DB 9; Length 407;

Best Local Similarity 100.0%; Pred. No. 7.2e-153;

Matches 407; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MGANTSRRPPVDFENEDVNFHFEILRAIGKSGFKVICVQKNDTKQYAMKYNKQKCV 60

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Db 121 ETVKLFICELVWALDYLNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETOITTM 180
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Db 181 AGTKPYMAPENFSSRGKAGYSFAVDWWSLGTAYELLGRPPYHRSSTSSKEIVHTFET 240
Qy 241 TVVTYPSAWSQEMVSLKLLLEPNPDQRFSDVQNFPPYMNNDINWDAVFKRLIPGFI 300
Db 241 TVVTYPSAWSQEMVSLKLLLEPNPDQRFSDVQNFPPYMNNDINWDAVFKRLIPGFI 300
Qy 301 NKGRLNCDDPTFELEEMILESPLHKKKKRLAKKEDMRKCDSSQTCLLQEHLDVQKEFI 360
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Qy 361 IFNREKVNDRDNKROPNLALQTKDPQVTNGQMDTGLSETFQTSKVS 407
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RESULT 2

US-10-620-845-9
; Sequence 9, Application US/10620845
; Publication No. US20040115693A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Nepomnichy, Boris
; APPLICANT: Wang, Xiaoming
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Walke, D. Wade
; TITLE OF INVENTION: Novel Human Kinase Proteins and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0167-USA
; CURRENT APPLICATION NUMBER: US/10/620,845
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US/09/841,683
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: US 60/199,499
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US 60/201,227
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 407
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-620-845-9

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RESULT 3
US-09-841-683-11
; Sequence 11, Application US/09841683
; Patent No. US20020081600A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Nepomnichy, Boris
; APPLICANT: Wang, Xiaoming
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Walke, D. Wade
; TITLE OF INVENTION: No. US20020081600A1 Human Kinase Proteins and Polynucleotides E
; FILE REFERENCE: LEX-0167-USA
; CURRENT APPLICATION NUMBER: US/09/841,683
; CURRENT FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: US 60/199,499
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US 60/201,227
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 396
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-841-683-11

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Best Local Similarity 99.2%; Pred. No. 4.6e-146;
Matches 389; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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RESULT 4
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; Sequence 20, Application US/10288798
; Publication No. US20030207299A1
; GENERAL INFORMATION:
; APPLICANT: BANDMAN, Olga; NGUYEN, Danniell B.;
; APPLICANT: WALIA, Narinder K.; HAFALIA, April J.A.;
; APPLICANT: YAO, Monique G.; GANDHI: Ameena R.;
; APPLICANT: GURURAJAN, Rajagopal; DING, Li;
; APPLICANT: PATTERSON, Chandra; YUE, Henry;
; APPLICANT: BAUGHN, Mariah R.; TRIBOULEY, Catherine M.;
; APPLICANT: THORNTON, Michael; ELLIOTT, Vicki S.;
; APPLICANT: LU, Yan; ISON, Craig H.;
; APPLICANT: AU-YOUNG, Janice; TANG, Y. Tom;
; APPLICANT: AZIMZAI, Yalda; BURRILL, John D.;
; APPLICANT: MARCUS, Gregory A.; ZINGLER, Kurt A.;
; APPLICANT: LU, Dyung Aina M.; LAL, Preeti G.;
; APPLICANT: RAMKUMAR, Javalaxmi; WARREN, Bridget A.;
; APPLICANT: KEARNEY, Liam; POLICKY, Jennifer L.;
; APPLICANT: THANGAVELU, Kavitha; BURFORD, Neil
; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCE: PI-0209 USA
; CURRENT APPLICATION NUMBER: US/10/288,798
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: PCT/US01/27219
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/240,542
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US 60/238,389
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 60/236,499
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 60/234,902
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US 60/232,654
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US 60/231,357
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: US 60/229,873
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PERL Program
; SEQ ID NO 20
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030207299A1 794584CD1
US-10-288-798-20

Query Match          95.8%; Score 2060; DB 14; Length 396;
Best Local Similarity 99.2%; Pred. No. 4.6e-146;
Matches 389; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Db 1 MGANTSRRKPPVFDENEDVNFDFEILRAIGKSGFGKVCIVQKNDTKQYAMKYNKQKCV 60

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Db 61 ERNEVRNVFKELQIMQGLEHFFLVNLWYSFQDEEDPMVVDLLGGDLRYHLOQNVHFKE 120

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Db 121 ETVKLFICELVMDLYLQNGRIIHRDMKPNILLDEGHVHIITDFNTAAMLPRETQITTM 180

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Db 181 AGTKPYMAPEMFSSRKAGAGYSFAVDWWSLGVATYELLGRRPYHIRSTSSKEIVHTFET 240

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US-10-362-892-20
; Sequence 20, Application US/10362892
; Publication No. US20040038881A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; BANDMAN, Olga
; APPLICANT: NGUYEN, Danniell B.; WALIA, Narinder K.
; APPLICANT: HAFALIA, April J.A.; YAO, Monique G.
; APPLICANT: GANDHI, Ameena R.; GURURAJAN, Rajagopal
; APPLICANT: DING, Li; PATTERSON, Chandra S.
; APPLICANT: YUE, Henry; BAUGHN, Mariah R.
; APPLICANT: TRIBOULEY, Catherine M.; THORNTON, Michael B.
; APPLICANT: ELLIOTT, Vicki S.; LU, Yan
; APPLICANT: ISON, Craig H.; AU-YOUNG, Janice K.
; APPLICANT: TANG, Y. Tom; AZIMZAI, Yalda
; APPLICANT: BURRILL, John D.; MARCUS, Gregory A.
; APPLICANT: ZINGLER, Kurt A.; LU, Dyung Aina M.
; APPLICANT: LAL, Preeti G.; RAMKUMAR, Javalaxmi
; APPLICANT: WARREN, Bridget A.; KEARNEY, Liam
; APPLICANT: POLICKY, Jennifer L.; THANGAVELU, Kavitha
; APPLICANT: BURFORD, Neil
; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCE: PF-0209 USN
; CURRENT APPLICATION NUMBER: US/10/362,892
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: PCT/US01/27219
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,873
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US 60/231,357
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: US 60/232,654
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US 60/234,902
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US 60/236,499
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 60/238,389
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 60/240,542
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PERL Program
; SEQ ID NO 20
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040038881A1 794584CD1
US-10-362-892-20

Query Match          95.8%; Score 2060; DB 15; Length 396;
Best Local Similarity 99.2%; Pred. No. 4.6e-146;
Matches 389; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MGANTSRRKPPVFDENEDVNFDFEILRAIGKSGFGKVCIVQKNDTKQYAMKYNKQKCV 60
Db 1 MGANTSRRKPPVFDENEDVNFDFEILRAIGKSGFGKVCIVQKNDTKQYAMKYNKQKCV 60

Qy 61 ERNEVRNVFKELQIMQGLEHFFLVNLWYSFQDEEDPMVVDLLGGDLRYHLOQNVHFKE 120
Db 61 ERNEVRNVFKELQIMQGLEHFFLVNLWYSFQDEEDPMVVDLLGGDLRYHLOQNVHFKE 120
```

Db 61 ERNEVRNVFKELQIMQGLEHFFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQNVHFKC 120
Qy 121 ETVKLFICELVMALDYLNQRIIHRDMKPDNILLDEGHVHITDFNIAAMLPRETOITTM 180
Db 121 ETVKLFICELVMALDYLNQRIIHRDMKPDNILLDEGHVHITDFNIAAMLPRETOITTM 180
Qy 181 AGTKPYMAPEMFSSRKAGYGFVADWWSLGVATYELLGRRPYHRSSTSSKEIVHTPET 240
Db 181 AGTKPYMAPEMFSSRKAGYGFVADWWSLGVATYELLGRRPYHRSSTSSKEIVHTPET 240
Qy 241 TVVTYPSAWSQEMVSLKLLLEPNDFQSFQSDVQNFPPYNDINWDAVFQKRLIPGIP 300
Db 241 TVVTYPSAWSQEMVSLKLLLEPNDFQSFQSDVQNFPPYNDINWDAVFQKRLIPGIP 300
Qy 301 NKGRNLCDPTFELEMILESKPLHKKKRLAKKEDMKRKCDSSTQCLLOEHLDSVQKEFI 360
Db 301 NKGRNLCDPTFELEMILESKPLHKKKRLAKKEDMKRKCDSSTQCLLOEHLDSVQKEFI 360
Qy 361 IFNREKVNDRDNFKQPNLALEQTKDPQVINGQ 392
Db 361 IFNREKVNDRDNFKQPNLALEQTKDPQGEDGQ 392

RESULT 6

US-10-182-243-33
; Sequence 33, Application US/10182243
; Publication No. US20040048310A1
; GENERAL INFORMATION:
; APPLICANT: FLOWMAN, GREGORY D.
; APPLICANT: WHITE, DAVID
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAN, SUCHA
; APPLICANT: MARTINEZ, RICARDO
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES AND PROTEIN KINASE-LIKE
; TITLE OF INVENTION: ENZYMES
; FILE REFERENCE: 038602/1366
; CURRENT APPLICATION NUMBER: US/10/182,243
; CURRENT FILING DATE: 2003-07-07
; PRIOR APPLICATION NUMBER: PCT/US01/02337
; PRIOR FILING DATE: 2001-01-25
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 33
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-243-33

Query Match 95.8%; Score 2060; DB 15; Length 396;
Best Local Similarity 99.2%; Pred. No. 4.6e-146;
Matches 389; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 MGANTSRRKPPVFDENEDVNFDFEILRAIGKSGFGKVCIVQKNDTKQWYAMKYNKQKCV 60
Db 1 MGANTSRRKPPVFDENEDVNFDFEILRAIGKSGFGKVCIVQKNDTKQWYAMKYNKQKCV 60
Qy 61 ERNEVRNVFKELQIMQGLEHFFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQNVHFKC 120
Db 61 ERNEVRNVFKELQIMQGLEHFFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQNVHFKC 120
Qy 121 ETVKLFICELVMALDYLNQRIIHRDMKPDNILLDEGHVHITDFNIAAMLPRETOITTM 180
Db 121 ETVKLFICELVMALDYLNQRIIHRDMKPDNILLDEGHVHITDFNIAAMLPRETOITTM 180
Qy 181 AGTKPYMAPEMFSSRKAGYGFVADWWSLGVATYELLGRRPYHRSSTSSKEIVHTPET 240
Db 181 AGTKPYMAPEMFSSRKAGYGFVADWWSLGVATYELLGRRPYHRSSTSSKEIVHTPET 240
Qy 241 TVVTYPSAWSQEMVSLKLLLEPNDFQSFQSDVQNFPPYNDINWDAVFQKRLIPGIP 300
Db 241 TVVTYPSAWSQEMVSLKLLLEPNDFQSFQSDVQNFPPYNDINWDAVFQKRLIPGIP 300
Qy 301 NKGRNLCDPTFELEMILESKPLHKKKRLAKKEDMKRKCDSSTQCLLOEHLDSVQKEFI 360

Db 301 NKGRNLCDPTFELEMILESKPLHKKKRLAKKEDMKRKCDSSTQCLLOEHLDSVQKEFI 360
Qy 361 IFNREKVNDRDNFKQPNLALEQTKDPQVINGQ 392
Db 361 IFNREKVNDRDNFKQPNLALEQTKDPQGEDGQ 392
RESULT 7
US-10-620-845-11
; Sequence 11, Application US/10620845
; Publication No. US20040115693A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Nepomniichy, Boris
; APPLICANT: Wang, Xiaoming
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Walke, D. Wade
; TITLE OF INVENTION: Novel Human Kinase Proteins and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0167-USA
; CURRENT APPLICATION NUMBER: US/10/620,845
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US/09/841,683
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: US 60/199,499
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US 60/201,227
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 396
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-620-845-11

Query Match 95.8%; Score 2060; DB 16; Length 396;
Best Local Similarity 99.2%; Pred. No. 4.6e-146;
Matches 389; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 MGANTSRRKPPVFDENEDVNFDFEILRAIGKSGFGKVCIVQKNDTKQWYAMKYNKQKCV 60
Db 1 MGANTSRRKPPVFDENEDVNFDFEILRAIGKSGFGKVCIVQKNDTKQWYAMKYNKQKCV 60
Qy 61 ERNEVRNVFKELQIMQGLEHFFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQNVHFKC 120
Db 61 ERNEVRNVFKELQIMQGLEHFFLVNLWYSFQDEEDMFVVDLLGGDLRYHLQNVHFKC 120
Qy 121 ETVKLFICELVMALDYLNQRIIHRDMKPDNILLDEGHVHITDFNIAAMLPRETOITTM 180
Db 121 ETVKLFICELVMALDYLNQRIIHRDMKPDNILLDEGHVHITDFNIAAMLPRETOITTM 180
Qy 181 AGTKPYMAPEMFSSRKAGYGFVADWWSLGVATYELLGRRPYHRSSTSSKEIVHTPET 240
Db 181 AGTKPYMAPEMFSSRKAGYGFVADWWSLGVATYELLGRRPYHRSSTSSKEIVHTPET 240
Qy 241 TVVTYPSAWSQEMVSLKLLLEPNDFQSFQSDVQNFPPYNDINWDAVFQKRLIPGIP 300
Db 241 TVVTYPSAWSQEMVSLKLLLEPNDFQSFQSDVQNFPPYNDINWDAVFQKRLIPGIP 300
Qy 301 NKGRNLCDPTFELEMILESKPLHKKKRLAKKEDMKRKCDSSTQCLLOEHLDSVQKEFI 360
Db 301 NKGRNLCDPTFELEMILESKPLHKKKRLAKKEDMKRKCDSSTQCLLOEHLDSVQKEFI 360
Qy 361 IFNREKVNDRDNFKQPNLALEQTKDPQVINGQ 392
Db 361 IFNREKVNDRDNFKQPNLALEQTKDPQGEDGQ 392

RESULT 8

US-10-410-764-101
; Sequence 101, Application US/10410764


```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Human
US-10-254-869-2

Query Match      95.2%; Score 2047; DB 14; Length 396;
Best Local Similarity 98.7%; Pred. No. 4.3e-145;
Matches 387; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGANTSRRKPPVFDENEDVNFDFEILRAIGKSGFKVCIVQKNDTKQYAMKYNKQKCV 60
DB 1 MGANTSRRKPPVFDENEDVNFDFEILRAIGKSGFKVCIVQKNDTKQYAMKYNKQKCV 60
QY 61 ERNEVRNVFKELQIMQGLEHPLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120
DB 61 ERNEVRNVFKELQIMQGLEHPLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120
QY 121 ETVKLFICELVMAIDYLNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTM 180
DB 121 ETVKLFICELVMAIDYLNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTM 180
QY 181 AGTKPYMAPEMFSSRKAGYSAVDWWSLGVATYELLGRPPYHRSSTSSKEIVHPTET 240
DB 181 AGTKPYMAPEMFSSRKAGYSAVDWWSLGVATYELLGRPPYHRSSTSSKEIVHPTET 240
QY 241 TVVTYPSAWSQEMVSLKLLKLEPNPDQRFSDVQNFPPYNDINWDVAFQKRLIPGIP 300
DB 241 TVVTYPSAWSQEMVSLKLLKLEPNPDQRFSDVQNFPPYNDINWDVAFQKRLIPGIP 300
QY 301 NKGRNLCDPTFELEEMILESPLHKKKRLAKKEMKMKCDSSQTCLLQEHLDVSQKEFI 360
DB 301 NKGRNLCDPTFELEEMILESPLHKKKRLAKKEMKMKCDSSQTCLLQEHLDVSQKEFI 360
QY 361 IFNREKVNDRDNKQPNALAEQTKDPQVINGQ 392
DB 361 IFNREKVNDRDNKQPNALAEQTKDPQVINGQ 392

RESULT 11
US-10-667-442-2
; Sequence 2, Application US/10667442
; Publication No. US20040043466A1
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CLO01160DIV II
; CURRENT APPLICATION NUMBER: US/10/667,442
; CURRENT FILING DATE: 2003-09-23
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-667-442-2

Query Match      95.2%; Score 2047; DB 15; Length 396;
Best Local Similarity 98.7%; Pred. No. 4.3e-145;
Matches 387; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGANTSRRKPPVFDENEDVNFDFEILRAIGKSGFKVCIVQKNDTKQYAMKYNKQKCV 60
DB 1 MGANTSRRKPPVFDENEDVNFDFEILRAIGKSGFKVCIVQKNDTKQYAMKYNKQKCV 60
QY 61 ERNEVRNVFKELQIMQGLEHPLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120
DB 61 ERNEVRNVFKELQIMQGLEHPLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120
QY 121 ETVKLFICELVMAIDYLNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTM 180
DB 121 ETVKLFICELVMAIDYLNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTM 180
QY 181 AGTKPYMAPEMFSSRKAGYSAVDWWSLGVATYELLGRPPYHRSSTSSKEIVHPTET 240
DB 181 AGTKPYMAPEMFSSRKAGYSAVDWWSLGVATYELLGRPPYHRSSTSSKEIVHPTET 240
QY 241 TVVTYPSAWSQEMVSLKLLKLEPNPDQRFSDVQNFPPYNDINWDVAFQKRLIPGIP 300
DB 241 TVVTYPSAWSQEMVSLKLLKLEPNPDQRFSDVQNFPPYNDINWDVAFQKRLIPGIP 300
QY 301 NKGRNLCDPTFELEEMILESPLHKKKRLAKKEMKMKCDSSQTCLLQEHLDVSQKEFI 360
DB 301 NKGRNLCDPTFELEEMILESPLHKKKRLAKKEMKMKCDSSQTCLLQEHLDVSQKEFI 360
QY 361 IFNREKVNDRDNKQPNALAEQTKDPQVINGQ 392
DB 361 IFNREKVNDRDNKQPNALAEQTKDPQVINGQ 392

RESULT 12
US-10-108-260A-267A
; Sequence 2674, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1el full length cDNA
; FILE REFERENCE: HI-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2674
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-267A

Query Match      84.9%; Score 1827; DB 15; Length 358;
Best Local Similarity 100.0%; Pred. No. 1.1e-128;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGANTSRRKPPVFDENEDVNFDFEILRAIGKSGFKVCIVQKNDTKQYAMKYNKQKCV 60
DB 1 MGANTSRRKPPVFDENEDVNFDFEILRAIGKSGFKVCIVQKNDTKQYAMKYNKQKCV 60
QY 61 ERNEVRNVFKELQIMQGLEHPLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120
DB 61 ERNEVRNVFKELQIMQGLEHPLVNLWYSFQDEEDMFVVDLLGGDLRYHLQONVHFKE 120
QY 121 ETVKLFICELVMAIDYLNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTM 180
DB 121 ETVKLFICELVMAIDYLNQRIIHRDMKPDNILLDEHGHVHITDFNIAAMLPRETQITTM 180
QY 181 AGTKPYMAPEMFSSRKAGYSAVDWWSLGVATYELLGRPPYHRSSTSSKEIVHPTET 240
DB 181 AGTKPYMAPEMFSSRKAGYSAVDWWSLGVATYELLGRPPYHRSSTSSKEIVHPTET 240
QY 241 TVVTYPSAWSQEMVSLKLLKLEPNPDQRFSDVQNFPPYNDINWDVAFQKRLIPGIP 300
DB 241 TVVTYPSAWSQEMVSLKLLKLEPNPDQRFSDVQNFPPYNDINWDVAFQKRLIPGIP 300
QY 301 NKGRNLCDPTFELEEMILESPLHKKKRLAKKEMKMKCDSSQ 344
DB 301 NKGRNLCDPTFELEEMILESPLHKKKRLAKKEMKMKCDSSQ 344

RESULT 13
US-10-074-978A-158
; Sequence 158, Application US/10074978A
; Publication No. US20040010119A1
; GENERAL INFORMATION:
; APPLICANT: Leite, Mario
```


protein kinase 2 (EC 2.7.1.1.-) - slime mold (Dictyostelium discoideum)
C:Species: Dictyostelium discoideum
C:Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 09-Jul-2004
C:Accession: A38578
R:Haribabu, B.; Dotti, R.P.
Proc. Natl. Acad. Sci. U.S.A. 88, 1115-1119, 1991
A:Title: Identification of a protein kinase multigene family of Dictyostelium discoideum
A:Reference number: A38578; MUID:91142122; PMID:11996312
A:Accession: A38578
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-479 <HAR>
A:Cross-references: UNIPROT:P28178; GB:M59744; NID:g167717; PID:AA33186.1; PID:g167718
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
C:Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; serine/threonine
F:151-407/Domain: protein kinase homology <KIN>
F:159-167/Region: protein kinase ATP-binding motif

Query Match 25.4%; Score 546; DB 2; Length 479;
Best Local Similarity 36.5%; Pred. No. 1.6e-17;
Matches 118; Conservative 66; Mismatches 123; Indels 16; Gaps 6;

Qy 11 VFEDN-EDVNFDFEILRAIGKSGFKVCIVQKNDTKMYAMKYNKQKCVNERVNVF 69
Db 140 IFSKNKQKATKDDPELLAVIGKSGFKYVQKKGEDKIFAMKVLKDAIARKQVNHK 199
Qy 70 KQLQIMQGLEHPFLVNLWYSFQDEDMFVVDLLGGDLRLYHLQNVHFKEETVKLFICE 129
Db 200 SEKTILOCSHPFVNLVHYATQDKLYVLDVFNGBELFHLKRGESPRVKIYAE 259
Qy 130 LVMLDYLQNRITHRDKMPNILLDEHGHVHTIDFNIAAMLPRETQITTMAGTKPYMAP 189
Db 260 IVSALDHLKQDIVYRDLKPNILLDSGHICITDFGLSKKIETTDGTFTCGTPPYLAP 319
Qy 190 EMFSRKAGYSFAVDWWSLGVATYELLRGRRPHIRSSSTSKSEIVHTFTVTVPYPSAW 249
Db 320 EVLN---GHGHCAGVDWWSLGLTYEMLTGLPPFYQNVSTMYQKILNGELKIPTY---I 373
Qy 250 SOEMVSLKLLPEPNDFQSFQSL---SDVQNPYPYNDINWDAVFOKRLIPGPFP---NGK 303
Db 374 SPEAKSLLEGLLTREVDKRLGTGGGEVQKQHPFNKIDWEKLDKREVEVHFKPKVKSSTD 433
Qy 304 RLNCDDPTFELE---EMILESRLP 323
Db 434 ISQIDPVFTQSRPMDSLVETSAL 456

RESULT 3
JQ1150
protein kinase (EC 2.7.1.37) cAMP-dependent, catalytic chain - slime mold (Dictyostelium
C:Species: Dictyostelium discoideum
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C:Accession: JQ1150
R:Buerki, E.; Anjard, C.; Scholder, J.C.; Raymond, C.D.
Gene 102, 57-65, 1991
A:Title: Isolation of two genes encoding putative protein kinases regulated during Dicty
A:Reference number: JQ1150; MUID:91323730; PMID:1864510
A:Accession: JQ1150
A:Molecule type: DNA
A:Residues: 1-648 <HUB>
A:Cross-references: UNIPROT:P34099; GB:M38703
C:Genetics:
A:Gene: PK2
A:Introns: 578/3
C:Complex: heterodimer with regulatory chain; active catalytic chain is released when cA
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
A:Note: important for cell type differentiation and fruiting body morphogenesis
C:Superfamily: Dictyostelium cAMP-dependent protein kinase catalytic chain; protein kinase
C:Keywords: ATP; magnesium; phosphoprotein; phosphotransferase; serine/threonine-specific
F:126-223/Region: glutamine-rich
F:297-312/Region: glutamine-rich
F:334-590/Domain: protein kinase homology <KIN>

F:342-350/Region: protein kinase ATP-binding motif
F:365,384,459,461/Active site: Lys, Glu, Asp, Lys #status predicted
F:464,468/Binding site: magnesium (Asn, Asp) #status predicted

Query Match 25.0%; Score 537.5; DB 1; Length 648;
Best Local Similarity 34.1%; Pred. No. 5e-17;
Matches 109; Conservative 74; Mismatches 120; Indels 17; Gaps 6;

Qy 9 PPVEDENEDVNFDFEILRAIGKSGFKVCIVQKNDTKMYAMKYNKQKCVNERVNV 68
Db 325 PPV---NARELKEFKQIRVLGTGTFGKVLQNTKGGCYAMKCLAKAYVQLKQVEHL 381
Qy 69 FKELQIMQGLEHPFLVNLWYSFQDEDMFVVDLLGGDLRLYHLQNVHFKEETVKLFICE 128
Db 382 NSEKILSSIIHPPIVNLVYQAFQDEKKLYLLFEVAGGEVFTHLRKSMSKFSNSTAKFYAA 441
Qy 129 ELVMALDYLQNRITHRDKMPNILLDEHGHVHTIDFNIAAMLPRETQITTMAGTKPYMA 188
Db 442 EIVLALDFLHKQNIYVRDLKPNILLDNQGHKIKTDFGAKRV---EDRTFTLCGTPEYLA 499
Qy 189 PEMFSRKAGYSFAVDWWSLGVATYELLRGRRPHIRSSSTSKSEIVHTFTVTVPYPSA 248
Db 500 PEITQSK---GHGKAVDWALGILIFEMLAGYPPFY---DDDTFAYINKILAGITPLG 553
Qy 249 WSQEMVSLKLLPEPNDFQSFQSL---DVQNPYPYNDINWDAVFOKRLIPGPFPKNGR 304
Db 554 FVDVDAKDLIKRLLTADTRRLGALKDQALDVGNHRWFSDINWERLYQRDNNGPPIPKIOH 613
Qy 305 LNCDDPTFELE---EMILESRLP 322
Db 614 QGDSNPFMYDEEMVEEPP 633

RESULT 4
S56639
ribosomal protein S6 kinase homolog (clone AspK11) - oat
N:Alternate names: mitogen-activated protein kinase pp70 homolog
C:Species: Avena sativa (Oat)
C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 16-Aug-2004
C:Accession: S56639
R:Huttly, A.K.; Phillips, A.L.
Plant Mol. Biol. 27, 1043-1052, 1995
A:Title: Gibberellin-regulated expression in oat aleurone cells of two kinases that show
A:Reference number: S56638; MUID:95284341; PMID:7766874
A:Accession: S56639
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-480 <HUT>
A:Cross-references: UNIPROT:Q43380; EMBL:X79992; NID:g871985; PIDN:CAA56313.1; PID:g871919
C:Superfamily: protein kinase homology
C:Keywords: ATP; phosphotransferase; protein kinase
F:149-407/Domain: protein kinase homology <KIN>
F:157-165/Region: protein kinase ATP-binding motif

Query Match 24.8%; Score 534; DB 2; Length 480;
Best Local Similarity 36.0%; Pred. No. 5.5e-17;
Matches 109; Conservative 61; Mismatches 123; Indels 10; Gaps 3;

Qy 14 ENEDVNFDFEILRAIGKSGFKVCIVQKNDTKMYAMKYNKQKCVNERVNVFKELQ 73
Db 142 ENEAVGLDNFELVKLVGGAGFYQYVRMKGTSIYAMKVMRKDKILEKNHAEYMKAEKD 201
Qy 74 IMQGLEHPFLVNLWYSFQDEDMFVVDLLGGDLRLYHLQNVHFKEETVKLFICEYMA 133
Db 202 ILTKVDHPFVQLRYSTQYKRLYLVDLVFNNGHLPFLYQOGLFRELARIYTAIEVSA 261
Qy 134 LDYLQNRITHRDKMPNILLDEHGHVHTIDFNIAAMLPRETQITTMAGTKPYMAPNFS 193
Db 262 VAHLHANGIMHRDLKPNILLDARGHAMLTDFGLAKEFDENTRSNMGCTVEYMAPEIV- 320
Qy 194 SRKAGYSFAVDWWSLGVATYELLRGRRPHIRSSSTSKSEIVHTFTVTVPYPSAQEM 253
Db 321 --QGRGHDKAADMWSVGILLFEMLTGKPPFF---GGNRDITQKIVREKMKLPSYLSSEV 375

Qy 254 VSLKLLLEPNPDQRFSSQ----LSDVQNPFPYNDINWDVAFQKRLIPGFIPIKGRNLNCDP 309
Db 376 HSLKGLLHKGAKRGLSGSDEIKHVKFWKAVNWKRLERQIQPSFCNVAQQTICIA 435
Qy 310 TFE 312
Db 436 NFD 438

RESULT 5
S68462
protein kinase ATPK6/ATPK1 (EC 2.7.1.1) - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 05-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 16-Aug-2004
A:Accession: S68462; A54141
R:Mizoguchi, T.; Hayashida, N.; Yamaguchi-Shinozaki, K.; Kamada, H.; Shinozaki, K.
FEBS Lett. 358, 199-204, 1995
A:Title: Two genes that encode ribosomal-protein S6 kinase homologs are induced by cold
A:Reference number: S68462; MUID:95129712; PMID:7828735
A:Accession: S68462
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-465 <MIZ>
A:Cross-references: UNIPROT:P42818; EMBL:D42056; NID:g667996; PIDN:BAA07656.1; PID:dl1008
R:Zhang, S.H.; Lawton, M.A.; Hunter, T.; Lamb, C.J.
J. Biol. Chem. 269, 17586-17592, 1994
A:Title: atpki, a novel ribosomal protein kinase gene from Arabidopsis. I. Isolation, ch
A:Reference number: A54141; MUID:94292519; PMID:7912697
A:Contents: ecotype Landsberg erecta
A:Accession: A54141
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-465 <ZHA>
A:Cross-references: GB:L29030; NID:g508307; PIDN:AAA21142.1; PID:g508308
A:Note: sequence extracted from NCBI backbone (NCBIN:149344, NCBI:P:149415)
C:Superfamily: protein kinase homolog
C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F:132-389/Domain: protein kinase homology <KIN>
F:140-148/Region: protein kinase ATP-binding motif

Query Match 24.6%; Score 529.5; DB 2; Length 465;
Best Local Similarity 34.8%; Pred. No. 8.4e-17;
Matches 104; Conservative 65; Mismatches 119; Indels 11; Gaps 3;
Qy 18 VNFDFHILRAIGSGFGKVCIVQKNTKQMYAMKMKQKVERNEVNFKEQLIQMG 77
Db 129 VGIDDFVMKVVGKAGFKVQVRKXETSEIYAMKMKDKHMEKNHAEYMKAEERDILTK 188
Qy 78 LEHFPVLNLYSFQDEEDMFVLDLGGDLRYHLQQNVHFKEETVKLFICELVWALDYL 137
Db 189 IDHPFIVQLKYSFQTKYRLYLVLDFINGGHLFFQLYHQGLFREDLARVYTAIEIVSAVSHL 248
Qy 138 QNQRILHRDMKPDNILLDEGHVHITDPNIAAALPRETOITTMAGTKPYMAPFSSRK 197
Db 249 HEKIMRDLAPENILMDTDGVMLTDFGLAKFEENTRSNMGCTTEYMAPEIV---RG 305
Qy 198 AGYSFVDWNSLGYATAYELLRGRPYHRSSTSSKEIVHTFTTVPYSAWSQEWVSL 257
Db 306 KGHDKAADWNSVGLLYEMLTGKPFGLSGKGIQKIV---KDKIKLPQLSNEAHAIL 361
Qy 258 KLLLEPNPDQ----FSQLSDVQNPFPYNDINWDVAFQKRLIPGFIPIKGRNLNCDPTE 312
Db 362 KGLLQKQEPERRGLSGLSGAEBIKQHKWFKGINWKKLEAREVMPSPFKPVSGRQCIANFD 420

RESULT 6
S37955
protein kinase YPK1 (EC 2.7.1.1) - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein YKL126w
C:Species: Saccharomyces cerevisiae
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 16-Aug-2004
C:Accession: S37955; A31248; S30903

R:Ramezani Rad, M.; Xu, G.; Kirchrath, L.; Fritz, C.; Keuchel, H.; Hollenberg, C.P.
submitted to the Protein Sequence Database, March 1994
A:Reference number: S37955
A:Accession: S37955
A:Molecule type: DNA
A:Residues: 1-680 <RAM>
A:Cross-references: UNIPROT:P12688; EMBL:Z28126; NID:g486212; PIDN:CAA81967.1; PID:g4862
A:Experimental source: strain S288C
R:Maurer, R.A.
DNA 7, 469-474, 1988
A:Title: Isolation of a yeast protein kinase gene by screening with a mammalian protein
A:Reference number: A31248; MUID:89090805; PMID:2850145
A:Accession: A31248
A:Molecule type: DNA
A:Residues: 1-200, 'L', 202-552, 'I', 554-680 <MAU>
A:Cross-references: EMBL:M21307; NID:gl72180; PIDN:AAA34880.1; PID:gl72181
R:Chen, P.; Lee, K.S.; Levin, D.E.
Mol. Gen. Genet. 236, 443-447, 1993
A:Title: A pair of putative protein kinase genes (YPK1 and YPK2) is required for cell gr
A:Reference number: S30903; MUID:93173125; PMID:8437590
A:Accession: S30903
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-200, 'L', 202-226, 'T', 228-552, 'I', 554-680 <CHE>
C:Genetics:
A:Gene: SGD:YPK1
A:Cross-references: SGD:S0001609; MIPS:YKL126w
A:Map position: 11L
C:Superfamily: protein kinase homolog
C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F:345-602/Domain: protein kinase homology <KIN>
F:353-361/Region: protein kinase ATP-binding motif
F:470/Active site: Asp #status predicted

Query Match 24.5%; Score 526; DB 2; Length 680;
Best Local Similarity 32.6%; Pred. No. 1.7e-16;
Matches 117; Conservative 77; Mismatches 123; Indels 42; Gaps 10;
Qy 8 KPPVFDENEDVNFDFHILRAIGSGFGKVCIVQKNTKQMYAMKMKQKVERNEV 67
Db 335 KP---SRNKPLSIDDFLLKVGSGFKVMQVRKDTQKYVALKAIKRSYIVSKSEVTH 391
Qy 68 VFKELOIQMGLEHPPVLNLYSFQDEEDMFVLDLGGDLRYHLQQNVHFKEETVKLFI 127
Db 392 TLAEITVLARVDCBFIVPLKFSFOSPEKLVFLAFINGGELFYHLQKEGRFDLSRRPYT 451
Qy 128 CELVWALDYLNQRIIHRDMKPDNILLDEGHVHITDPNIAAALPRETOIT-TMAGTKPY 186
Db 452 AELLCALDNLHLKLDVVYRDLPENILLDYQGHIALCDFGLCKLNKDDKDTDTFCGTPEY 511
Qy 187 MAPFMFSRRKAGYSFVDWNSLGYATAYELLRGRPYHRSSTSSKEIVHTFTTV----V 243
Db 512 LAPELL---LGLGYTKAVDWMTLGVLLYEMLTGLPPYY-----DEDVPMVKKILQSP 562
Qy 244 TYPASQEWVSLKLLLEPNPDQ---FSQLSDVQNPFPYNDINWDVAFQKRLIPGFI 301
Db 563 VFPDGFDRDKDLIGLLSLRDPTRLRGYNGADEIRNHFFFSQLSWKRLMKGYIPPYKPA 622
Qy 302 KGRNLNCDPTELEBEMILESPLHKKKRLAKKEDKMKCDSSQTCLLQEHLL-DSVQKEF 359
Db 623 VS--NSMDTSNFDDEFTREKPI-----DS----VDEYLSESVQKQF 658

RESULT 7
C31751
protein kinase (EC 2.7.1.37), CAMP-dependent, catalytic chain - fruit fly (Drosophila me
C:Species: Drosophila melanogaster
C:Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 09-Jul-2004
C:Accession: C31751; A28269
R:Kalderson, D.; Rubin, G.M.
Genes Dev. 2, 1539-1556, 1988
A:Title: Isolation and characterization of Drosophila cAMP-dependent protein kinase gene
A:Reference number: A31751; MUID:89107990; PMID:3215511

A;Accession: C31751
A;Molecule type: DNA
A;Residues: 1-353 <KAL>
A;Cross-references: UNIPROT:P12370; EMBL:X16969; NID:g7806; PIDN:CAA34840.1; PID:g7807;
R;Foster, J.L.; Higgins, G.C.; Jackson, F.R.
J. Biol. Chem. 263, 1676-1681, 1988
A;Title: Cloning, sequence, and expression of the Drosophila cAMP-dependent protein kinase
A;Reference number: A92684; MUID:88115281; PMID:2828348
A;Accession: A28269
A;Molecule type: DNA
A;Residues: 2-353 <FOS>
A;Cross-references: GB:M18655; GB:J03504; NID:g157051; PIDN:AAA28412.1; PID:g157052
C;Genetics:
A;Gene: FlyBase:PkA-C1
A;Cross-references: FlyBase:PBgn0000273
C;Superfamily: Kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; blocked amino end; cAMP binding; heterotrimer; lipoprotein; magnesium
F;2-353/Product: protein kinase, cAMP-dependent, catalytic chain #status predicted <MAT>
F;44-300/Domain: protein kinase homology <KIN>
F;52-60/Region: protein kinase ATP-binding motif
F;72/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;72/Modified site: aspartic acid (Asn) #status predicted
F;57,58,124,130,173,186/Binding site: Mg-ATP (Phe, Gly, Glu, Glu, Thr) #status predicted
F;75,94,169,171/Active site: Lys, Glu, Asp, Lys #status predicted
F;174,187/Binding site: magnesium (Asn, Asp) #status predicted
F;200/Binding site: phosphate (Thr) (covalent) #status predicted
F;341/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 24.2%; Score 521.5; DB 2; Length 353;
Best Local Similarity 34.7%; Pred. NO. 1.5e-16;
Matches 111; Conservative 73; Mismatches 117; Indels 19; Gaps 6;
QY 21 DHEFTLRAIGKSGFKGVCIVQKNDTKKMYKMKQKVERNEVRNVFKELQIMQGLEH 80
DB 44 DFERIKLTGSGFVGMVIOHKPKDYAMKILQKQVKLKQVEHTLNEKRILQALQF 103
QY 81 PELVNLVTSFQDEDMFMVVDLLGLDRLYLQNVHFEKTEVKLFCICELVMDLYLQ 140
DB 104 PFLVSLRVHFKDNLNLYLVVPGEMFSLRKVGREFSEHRSFYAAQIVLAPEYLHYL 163
QY 141 RIHRMDKPDNLLDEHGHVHTIDFNIAAMLPRETOITMAGTKPYMAPESSEKAGY 200
DB 164 DLIVRLDKPENLLDSQGYLVKTDGFAKRVKGR--WTLCGTPEYLAPEILSK--GY 218
QY 201 SFADVWSLGVTAELLGRRRYHRSSTSSKEIVHTETTV---VTVPSSAWSQBMVSL 257
DB 219 NKADVWALGVLVENAGYPPFP-----ADQPIQVEKIVSGKVRFPSPHSGDLKDL 272
QY 258 KKLLENPDQRFSQL-----SDVQNFPPYMDINWDVQKRLIPGIPN-KGRNLCDPTFE 312
DB 273 RNLLQVLDLTKRYGNLKAGVNDIKNQKWPASTDIAIFOKKIEAPIPRCKGPGDTSNPD 332
QY 313 LSEEMILESPLHKKKRLAK 332
DB 333 YBEALRLISSTKCAKEFAE 352

RESULT 8
S68463
protein kinase ATPK19 (EC 2.7.1.1) - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 05-Dec-1996 #sequence_revision 27-Feb-1997 #text_change 16-Aug-2004
C;Accession: S68463
R;Mizoguchi, T.; Hayaashida, N.; Yamaguchi-Shinozaki, K.; Kamada, H.; Shinozaki, K.
FEBS Lett. 358, 199-204, 1995
A;Title: Two genes that encode ribosomal-protein S6 kinase homologs are induced by cold
A;Reference number: S68462; MUID:95129712; PMID:7828736
A;Accession: S68463
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-471 <MTZ>
A;Cross-references: UNIPROT:Q39030; EMBL:D42061; NID:g1526412; PIDN:BAA07661.1; PID:d100
C;Superfamily: protein kinase homology

C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F;138-395/Domain: protein kinase homology <KIN>
F;146-154/Region: protein kinase ATP-binding motif

Query Match 24.2%; Score 521; DB 2; Length 471;
Best Local Similarity 34.0%; Pred. NO. 2e-16;
Matches 108; Conservative 63; Mismatches 123; Indels 24; Gaps 4;

QY 12 FDSEED-----VNFDFEILRAIGKSGFKGVCIVQKNDTKKMYKMKQK 58
DB 116 FSGNDTDEKSPPEEVGVVIGIEFVLKVGQAGFKVQVVRKDTSEIYAMKVMKDK 175
QY 59 CVERNEVRNVFKELQIMQGLEHFFLVNLYSFODEDMFMVVDLLGLDRLYLQNVH 118
DB 176 IVEKNAEYKMAERDILTKIDHPFIVQLKYSFQTKRYLYLVLDINGHLPFOLYHOG 235

QY 119 KEETVKLFCICELVMDLYLQNVRIHRDMKPDNLLDEHGHVHTIDFNIAAMLPRETOIT 178
DB 236 REDLARVYTAIVSVVSHLHEKGIMHRDLKPENLMDVGHVMTDGLAKFEENTRSN 295

QY 179 TMAGTKPYMAPENFSRKGAGYSFADVWMSLGVTAELLGRRRYHRSSTSSKEIVHTF 238
DB 296 SMCGTTEYMAPEIV---RGKHDKAADWSVGLLYEMLTGKPPFLSGSKGIQKIV--- 349

QY 239 ETTVTVPSSAWSQBMVSLKLLLEPNPDQRF-----SQLSDVQNFPPYMDINWDVQKRL 294
DB 350 -KDKIKLPQVFVNEAHALLKGLQKEPERRLGSFGSGABEIKKHKWFKAINWKKLEAREV 408

QY 295 IPGFIPNKGRLNCDPTFE 312
DB 409 QPSFKPAVSGRQCIANPD 426

RESULT 9

S55694
protein kinase (EC 2.7.1.37) sck1, cAMP-dependent - fission yeast (Schizosaccharomyces p
C;Species: Schizosaccharomyces pombe
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 16-Aug-2004
C;Accession: S55694; T38040
R;Jin, M.; Fujita, M.; Cullley, B.M.; Apolinaro, E.; Yamamoto, M.; Maundrell, K.; Hoffma
Genetics 140, 457-467, 1995
A;Title: sck1, a high copy number suppressor of defects in the cAMP-dependent protein ki
A;Reference number: S55694; MUID:96120227; PMID:7498728
A;Accession: S55694
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-696 <JIN>
A;Cross-references: UNIPROT:P50530; GB:D38108; NID:g1136301; PIDN:BAA07286.1; PID:d10078
A;Note: the authors translated the codon GAT for residue 687 as His
R;McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Whitehead, S.; Churcher, C.M.
submitted to the EMBL Data Library, August 1999
A;Reference number: Z21764

A;Accession: T38040

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-176, 'F', 178-198, 'A', 200-696 <MCD>

A;Cross-references: EMBL:AL109951; PIDN:CA83053.1; GSPDB:GN00066; SPDB:SPAC1B9.02c

A;Experimental source: strain 972h-; cosmid c1B9

C;Genetics:

A;Gene: sck1; SPDB:SPAC1B9.02c

A;Map position: 1

A;Insertion: 80/3; 311/1; 633/2

C;Superfamily: protein kinase homology

C;Keywords: ATP; phosphotransferase; protein kinase

F;308-316/Region: protein kinase ATP-binding motif

QY 11 VFDEDEDYVNF--DFEFTLRAIGKSGFKGVCIVQKNDTKKMYKMKQKVERNEVRNV 68

Query Match 24.2%; Score 519.5; DB 2; Length 696;

Best Local Similarity 37.2%; Pred. NO. 3.3e-16;

Matches 112; Conservative 63; Mismatches 111; Indels 15; Gaps 7;

Db 288 IVEHIEHVRYGPEDTALRLICKGTGQVVLVRKNDTNRIYAMKKISKLLIVRKKEVTHT 347
Qy 69 PKEIQIMOGL---EHPFLVNLWYSFQDEEDFMVVDLLGGDLRYHLQONVHFKEETVKL 125
Db 348 LGERNILVRLTSLDESPPFVIGLKFSQASDLYLTDYMSGGELFMHLOHEGRFPPEORAKF 407
Qy 126 FICELVMAVDYLNQRIIHRDMKPDNILLDEGHVHITDFNIA-AMLPRETQITTMAGTK 184
Db 408 YIAELVLALEHLKHDIYRLKPNENILLDADGHIALCDFGLSKANLSANATTWFFCGTT 467
Qy 195 PYMAPESPSSRKAGYSFAVDWMSLGVATYELLRRRPPYHRSSTSSKEIVHTTETTVT 244
Db 468 EYLAPVLELDEK--GYTKQVDFWSLGVLFVEMCCGWSFPY---APDVQVMRYNIAFGKVR 522
Qy 245 YP-SAWSEMVSLLKLEPNPDQFQSLSD---VONFPYVNDINWDAVFOKRLIPGP 300
Db 523 FPKGVLSSEGRSFVRGLLRNPNHRLGAVADTTTELKEHPFFADINWDLSSKKKQVPPPKP 582
Qy 301 N 301
Db 583 N 583
RESULT 10
T20232
hypothetical protein C54G4.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T20232
R;Wilkinson, J.
submitted to the EMBL Data Library, June 1996
A;Reference number: Z19241
A;Accession: T20232
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-785 <WIL>
A;Cross-references: UNIPROT:Q18846; EMBL:Z75533; PIDN:CAA99814.1; GSPDB:GN00019; CESP:CS54G4
A;Experimental source: clone CS4G4
C;Genetics:
A;Gene: CESP:C54G4.1
A;Map position: 1
A;Introns: 55/3; 188/2; 237/2; 339/3; 397/2; 474/3; 504/3; 558/2; 594/3; 687/1; 736/2
C;Superfamily: ribosomal protein S6 kinase II; protein kinase homology
Query Match 24.2%; Score 519.5; DB 2; Length 785;
Best Local Similarity 37.0%; Pred. No. 3.6e-16;
Matches 111; Conservative 72; Mismatches 106; Indels 11; Gaps 8;
Qy 14 ENEDVNFDFEILRAIGKSGFKVCIVOK---NDTKMYAMKYNKQKCVNERE-VRNVP 69
Db 8 EGEKVSMEFNALLRVLGKYGAYKFLVRKVGKGKDHNTIYAMKVLKTRVLTKQKTLBHTM 67
Qy 70 KELYQIMOGL-HPFLVNLWYSFQDEEDFMVVDLLGGDLRYHLQONVHFKEETVKLFIC 128
Db 68 AERQVLERLGTFFLVNLFPYAFQDTDKLHYVYRGGELTHLCRSHGFDEARFVIA 127
Qy 129 ELVMAVDYLNQRIIHRDMKPDNILLDEGHVHITDFNIAAM-LPRE-TQITTMAGTKPY 186
Db 128 ELVVAIDSLHQKVIYRDLKLENILLDEGHVKLTDFGLSKLFLPGELDRANSYCGTIEY 187
Qy 187 MAPEMFSSRKAGYSFAVDWMSLGVATYELLRRRPPYHRSSTSSKEIVHTTETTVTY 245
Db 188 MSPEVINRPEG-GYSDVVDWMSLGVISFELLTGCSPTVDGAQNSKDKIAKRIYTKKVPF 246
Qy 246 PSAMSQEMVSLLKLEPNPDQ---FSQSLSDVONFPYVNDINWDAVFOKRLIPGFINKG 303
Db 247 PXTMDVDARDFIGQLLEKLEKRLGNGVDIEKNHFMSSIDWDAAVKRLKPVIVFRIG 306

RESULT 11
S19027
protein kinase A (EC 2.7.1.1-) catalytic chain - California sea hare
C;Species: Aplysia californica (California sea hare)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S19027
R;Beushausen, S.; Bergold, P.; Sturmer, S.; Elste, A.; Roytenberg, V.; Schwartz, J.H.; B
Neuron 1, 853-864, 1988
A;Title: Two catalytic subunits of cAMP-dependent protein kinase generated by alternativ
A;Reference number: S19027; MUID:90166564; PMID:2483106
A;Accession: S19027
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-352 <BSU>
A;Cross-references: UNIPROT:Q16957; EMBL:X63420; NID:G5576; PIDN:CAA45014.1; PID:G5577
as Glu, CTA for residue 271 as Glu, AAC for residue 285 as Asp, and AAC for residue 288
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: phosphotransferase
F;42-299/Domain: protein kinase homology <KIN>
Query Match 24.1%; Score 518; DB 2; Length 352;
Best Local Similarity 33.6%; Pred. No. 2.1e-16;
Matches 109; Conservative 83; Mismatches 102; Indels 30; Gaps 10;
Qy 21 DHFEILRAIGKSGFKVCIVQ-KNDTKMYAMKYNKQKCVNERVNVFKELQIMOGL 79
Db 42 DDPDRINTLGTGSGFVRVNLVQHKESRNFYAMKILDKQVVKLQVHTEKILQISIN 101
Qy 80 HPFLVNLWYSFQDEEDFMVVDLLGGDLRYHLQONVHFKEETVKLFICELVMAVDYLN 139
Db 102 FPFVLKLEYFKDQNSLYMVLFTVGTGEMFSLHRRIGRFSRPHSRFVAAQIVLVLEYLHH 161
Qy 140 QRIIHRDMKPDNILLDEGHVHITDFNIAAMLPRETQITTMAGTKPYMAPEMFSSRKAG 199
Db 162 LDIMYRLKPNENILLDSDYGLKVTDFGAKVKQRT--WTLCGTPEYLAPEIILSK--G 216
Qy 200 YSFAVDWMSLGVATYELLRRRPPYHRSSTSSKEIVHTTETTV---VTYPSAWSQEMVSL 256
Db 217 YNKAVDWALGVLIYEMAAGVPPPF-----ADQPIQIYEKIVSGKVRFSHFSSDLKDL 270
Qy 257 LKLEPNPDQFQSL-----SDVONFPYVNDINWDAVFOKRLIPGFIP-NIGRLNCDPTF 311
Db 271 LRNLQVLDLTKRFGNLKNGVNDIKNHKWFSTTDIAIYQKRVKVEAPFVPTKKG---AGDTA 327
Qy 312 ELBEMILESPLHKKKRLAKKEK 335
Db 328 NFDD--YEEPEL-----RISSTEK 344
RESULT 12
T21211
hypothetical protein ZK909.2a - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21211; T28100
R;McLay, K.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19391
A;Accession: T21211
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-359 <WIL>
A;Cross-references: UNIPROT:P21137; EMBL:Z81511; PIDN:CAB04168.1; GSPDB:GN00019; CESP:ZK
R;White, S.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z20469
A;Accession: T28100
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-359 <WIL>
A;Cross-references: EMBL:Z82096; PIDN:CAB05034.1; GSPDB:GN00019; CESP:ZK909.2a
A;Experimental source: clone ZK909
C;Genetics:
A;Gene: CESP:ZK909.2a
A;Map position: 1

A; Introns: 24/1; 44/3; 87/3; 120/3; 190/3; 318/3
C; Superfamily: kinase-related transforming protein; protein kinase homology

	Query Match	24.0%;	Score 517;	DB 2;	Length 359;
	Best Local Similarity	33.3%;	Pred. No. 2.4e-16;		
	Matches 110;	Conservative 79;	Mismatches 119;	Indels 22;	Gaps 7;
Qy	14	ENEDVN----	PDHFEILRAIGKSGFGVCIVOKNDTKKMYAMKYMKNQKQKVERNEVRNVEK	70	
Dd	40	ENPAQNTACLDLDDPRIKTLTGSGFGRVWLVKHKQSGNYAMKILDKQVKVLKQVEHTLN	99		
Qy	71	ELQIMQGLEHPFLVNLWYSPQDEDMFVVDLLGGLRLYLQONVHFKEETVKLFICEL	130		
Dd	100	EKRILQAIDPFVLVNMVTFSPKDNSLVMVLEFTSGGEMFSLNRRIKGFSEPHSRFPYAAQI	159		
Qy	131	VMALDYLYONQRIIHRMDKPNILLDHGHHVITDFNIAAMLPRETOITTMAGTKPYAPE	190		
Dd	160	VLAPEYLHLDLYRLDKPENLLIDSTGYLIKITDFGFAKRVKGR--WTLCGPPEYLAPE	217		
Qy	191	MFPSRKAGYSFAVDWMSLGVATAYELLRRRPHIRSSSTSSKEIVHTFTTV----	247		
Dd	218	IILSK-----GYNKAVDMWALGVLYIEMAAGVPPPF-----ADQPIQIYEKIVSGKVKFP	268		
Qy	248	AWSOEYMSLLKLLLEPNPDFQSFQL-----SDVQNFPYMDINWDVAFQKELIPGFI	302		
Dd	269	HFSNELKDLLNVLLOVDLTKRYGNLKNGVADIKNHKWFSGSTDMIAIYQKIEAPFLPKCR	328		
Qy	303	GRLNCDPTFLEEMILSKPLHKKKKRLAK	332		
Dd	329	GGPDASNFDDYEEEPRLISGTETKCAKEFAE	358		

RESULT 13

I38556
 Ribosomal protein S6 kinase 2 (EC 2.7.1.1) 3 - human
 N/Alternate names: Insulin-stimulated protein kinase 1 (PK-1, ISPK1); MAP kinase-activated
 C/Species: Homo sapiens (man)
 C/Date: 06-Sep-1996 #sequence Revision 06-Sep-1996 #text_change 09-Jul-2004
 C/Accession: I38556, I64835
 R/Bjorbaek, C.; Vik, T.A.; Echwald, S.M.; Webb, G.C.; Wang, J.P.; Yang, P.Y.; Vestergaard
 Diabetes 44, 90-97, 1995
 A/Title: Cloning of a human insulin-stimulated protein kinase (ISPK-1) gene and analysis
 nts.
 A/Reference number: I38556; MUID: 95113220; PMID: 7813820
 A/Accession: I38556
 A/Status: preliminary; translated from GB/EMBL/DBDJ
 A/Molecule type: mRNA
 A/Residues: 1-740 <EO>
 A/Cross-references: UNIPROT:P51812; EMBL:U08316; NID:q475587; PIDN:AAA81952.1; PID:g4755
 R/Moller, D.E.; Xia, C.H.; Tang, W.; Zhu, A.X.; Jakubowski, M.
 Am. J. Physiol. 266, 351-359, 1994
 A/Title: Human risk isoforms: cloning and characterization of tissue-specific expression.
 A/Reference number: I51901
 A/Accession: I64835
 A/Status: preliminary; translated from GB/EMBL/DBDJ
 A/Molecule type: mRNA
 A/Residues: 2-423, 'L', 425-479, 'N', 481-493, 495-582 <MOL>
 A/Cross-references: GB:L07601; NID:G401773; PIDN:AAC82495.1; PID:g401774
 C/Comment: Although ribosomal protein S6 (see PIR:R3HU6) is phosphorylated by this enzym
 C/Genetics:
 A/Gene: GDB:RPS6K3; RSK; HU-2; RSK2; HU-3
 A/Cross-references: GDB:365648; OMIM:300075
 A/Map position: Xp22.2-Xp22.2
 C/Supfamily: ribosomal protein S6 kinase II; protein kinase homology
 C/Keywords: ATP; monomer; phosphoprotein; phosphotransferase; serine/threonine-specific
 P:66-327/Domain: protein kinase homology <KIN1>
 P:74-82/Region: protein kinase ATP-binding motif
 P:420-679/Domain: protein kinase homology <KIN2>
 P:428-436/Region: protein kinase ATP-binding motif
 Query Match 23.9%; Score 514.5; DB 2; Length 740;
 Best Local Similarity 35.8%; Pred. No. 5.7e-16;
 Matches 112; Conservative 65; Mismatches 117; Indels 19; Gaps 7;

RESULT 14

A:Species: Saccharomyces cerevisiae
A:Title: The SCH9 protein kinase mRNA contains a long 5' leader with a small open reading frame
A:Accession: S30022; MUID:93182531; PMID:8442384
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-823 <WAC>
A:Cross-references: UNIPROT:P11792; EMBL:U00029; NID:g551322; PIDN:AAB69735.1; PID:g4589
R:di Blasi, F.; Carra, E.; de Vendittis, E.; Masturzo, P.; Burderi, E.; Lambrinoudaki, I.
Yeast 9, 21-32, 1993
A:Title: The SCH9 protein kinase mRNA contains a long 5' leader with a small open reading
A:Reference number: S30021
A:Accession: S30022
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 'M', 1-823 <DIB>
A:Cross-references: EMBL:X57629; NID:g5277; PIDN:CAA40853.1; PID:g5279
A>Note: The nucleotide sequence was submitted to the EMBL Data Library, February 1991
R:Toda, T.; Cameron, S.; Sass, P.; Wigler, M.
Genes Dev. 2, 517-527, 1988
A:Title: SCH9, a gene of Saccharomyces cerevisiae that encodes a protein distinct from,
Genes Dev. 2, 517-527, 1988

A:Accession: A428423
 A:Molecule type: DNA
 A:Residues: 'M', 1-364, 'S', 366-749, 'K', 751-823 <TOD>
 A:Cross-references: EMBL:X12560; NID:G4425; PIDN:CAA31073.1; PID:G4426
 C:Genetics:
 A:Gene: SGD:SCH9
 A:Cross-references: SGD:S0001248; MIPS:YHR205W
 A:Map position: 8R
 C:Superfamily: protein kinase homology
 C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
 F:409-670/Domain: protein kinase homology <KIN>
 F:417-425/Region: protein kinase ATP-binding motif

 Query Match 23.9%; Score 514.5; DB 2; Length 823;
 Best Local Similarity 31.5%; Pred. No. 6.3e-16;
 Matches 139; Conservative 81; Mismatches 156; Indels 65; Gaps 15;

 QY 6 SRKSPVFEDE--NEDVNF-----DHFELRAIGKSGFKVCIVQKNDTKKMY 49

Db 378 SLKPRVDEVVSGDILIKWTYKQTKRHYGPDQEVLELLGKTFGGVYQVKKDQRIY 437
Qy 50 AMKYNKQKVERNEVRNVFELQIM---QGLEHPFLVNLWYSQDDEDMVVDLLGG 106
Db 438 AMKVLSSKVIYKQNEIAHTIGERNILVTTASKSPFIVGLKFSQTPDLYLVTDYMSGG 497
Qy 107 DLRYHLQONVHFKEETVKLFCELVMDLYLQONQRIIHRDMKPDNILLDEHGHVHTDEN 166
Db 498 ELFWHLQREGRFSDRAKFIAEVLVLALEHLDNDIVTRDUPENILLDANGNIALCDFG 557
Qy 167 IA-AMLPRETQITTMAGTKPMAPEMFSSRRKAGYSFAVDMWSLGVTAAYELLRRRYPYHI 225
Db 558 LSKADLKDRT--NTFCGTTEVLAPELLLDE--TCYTKVDFWLSGLVLFEMCCWSPPF- 612
Qy 226 RSSTSSKEIVHTPTTWTYP-SAWSQEMVSLKLLLEPNPDQRFPSQLSD---VONFPYM 281
Db 613 --AENNOVMYQKIAFGKVKFPRDVLSEGRSFVKGLLRNPKHRLGAIDDDGRLRAHPFF 670
Qy 282 NDINWDAVFOKRLIPGFIPTN---KGRINCDDPTF-----ELEEMLSKPLHKKKR 329
Db 671 ADIDWEALKOKKIPPPKPHLVSTDTSNFDPETTASTSYMNKHQPMMTATPL---SPA 727
Qy 330 LAKEKDMRKCDSSQTCLLQHLDSVQK-----EPIIFN-----REKVNRFNK 373
Db 728 MQAKFAGTTFVDES---AIDEHVNNRKFLQNSYFMEPGSFIPGNPLPPDEDVIDDDGD 784
Qy 374 RQPNLALEQTKDPQVTVNGMD 394
Db 785 EDINDGFNOEKMNNSHSD 805

RESULT 15

T21212
hypothetical protein ZK909.2b - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T21212; T28101
R:McLay, K.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19391
A:Accession: T21212
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-375 <WIL>
A:Cross-references: UNIPROT:P21137; EMBL:Z81511; PIDN:CAB04169.1; GSPDB:GN00019; CESP:ZK909.2b
A:Experimental source: clone F21F12
R:White, S.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z20469
A:Accession: T28101
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-375 <W12>
A:Cross-references: EMBL:Z82096; PIDN:CAB05035.1; GSPDB:GN00019; CESP:ZK909.2b
A:Experimental source: clone ZK909
C:Genetics:
A:Gene: CESP:ZK909.2b
A:Map position: 1
A:Introns: 24/1; 44/3; 87/3; 120/3; 130/3; 318/3
C:Superfamily: kinase-related transforming protein; protein kinase homology

Query Match 23.9%; Score 514; DB 2; Length 375;
Best Local Similarity 34.7%; Pred. No. 3.3e-16;
Matches 105; Conservative 75; Mismatches 101; Indels 22; Gaps 7;
Qy 14 ENEDVN---FDHFEILRAIGKSGFKGKVICIVKNDTKQYAMKYNKQKVERNEVRNVFK 70
Db 40 ENPAQNTACLDPDFRIKTLGTGSGFRVNLVKHKGSGNYAMKILDOKVVKLKQVEHTLN 99
Qy 71 ELQIMQGLEHPEFLVNLWYSQDEEDMVDLLGGDLRYHLQONVHFKEETVKLFCEL 130
Db 100 EKRLQAIIDFPFLVNMFTSFKDNLSNLYMVLEFISGEMFSLHRRIGRFPSEPHSRFYAAQI 159

Qy 131 VMALDYLQONQRIIHRDMKPDNILLDEHGHVHTDENIAAMLPRETOITTMAGTKPYMAPE 190
Db 160 VLAPEYLSLDLYRDLKPNELLIDSTGYLKITDGFAGKRVKGRV--WTLCGTPEYLAPE 217
Qy 191 MFSRRKAGYSFAVDMWSLGVTAAYELLRRRYPYHIRSSTSSKEIVHTPETTV---VTYPS 247
Db 218 IILSK---GYNKAVDWALGVLIYEMAAGYPPFF-----ADQPIQIYEKIVSGVKVFP 268
Qy 248 AWSQEMVSLKLLLEPNPDQRFPSQLSD---SDVQNFPMNDINWDAVFOKRLIPGFI 303
Db 269 HFSNELKDLLKNLLIQVDLTKRYGNLKNGVADIKNKKWFGSTDMIAIYQKKITPPSPF-SKG 327
Qy 304 RLN 306
Db 328 ESN 330

Search completed: December 17, 2004, 09:28:44

Job time : 41 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 17, 2004, 09:25:19 ; Search time 74 Seconds

(without alignments)

3164.561 Million cell updates/sec

Title: US-10-620-845-9

Perfect score: 2151

Sequence: 1 MGNTSRKPPVFEDENEDVNF.....VTNQMOTGLSETFQTSKVS 407

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 02:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1880	87.4	398	2	QB6GW6 m mus muscu
2	1707	79.4	368	2	Q7TPQ4 mus musculus
3	1527	71.0	396	2	Q6GQ72 xenopus lae
4	1441	67.0	414	2	Q9JXJ8 mus musculus
5	1438.5	66.9	414	2	Q7TMD3 mus musculus
6	1438.5	66.9	414	2	AH58412 mus muscu
7	1434.5	66.7	414	2	Q8C4E0 mus musculus
8	1423.5	66.2	414	2	Q9NY57 mus musculus
9	1419.5	66.0	414	2	Q8IY14 homo sapien
10	1333.5	62.0	488	2	Q9JJG4 mus musculus
11	1333.5	62.0	488	2	Q8QZV4 mus musculus
12	1332.5	61.9	486	2	Q86UX6 mus musculus
13	1186.5	55.2	364	2	Q8UXH3 mus musculus
14	1186.5	55.2	364	2	AAQ88719 mus muscu
15	1142	53.1	369	2	Q86UB1 mus musculus
16	1127.5	52.4	368	2	Q9BGT4 macaca fasc
17	910	42.3	333	2	Q7QFG8 anopheles g
18	852.5	39.6	379	2	Q21483 caenorhabdi
19	835	38.8	166	2	Q8WU08 homo sapien
20	714.5	33.2	700	2	Q9VN23 drosophila
21	684	31.8	367	2	Q96WJ8 blumeria gr
22	595.5	27.7	444	1	KKAC.DICDI
23	561.5	26.1	446	2	Q6PLK2 dictyosteli
24	561.5	26.1	446	2	AA06260 plasmodiu
25	561.5	26.1	735	2	Q8I4W3 plasmodiu
26	546	25.4	479	1	PK2.DICDI
27	537.5	25.0	648	1	KAPC.DICDI
28	537.5	25.0	683	2	Q6C936 varrowia li
29	534	24.8	480	2	Q43380 avena sativ
30	533.5	24.8	704	2	Q8FMJ9 candida gla
31	532	24.7	471	1	Q39030 arabidopsis

32	531	24.7	703	2	O6FN22
33	529.5	24.6	465	1	KPK1_ARATH
34	529.5	24.6	465	2	AA138706
35	529.5	24.6	465	2	AA20205
36	529	24.6	456	2	Q8MYF1
37	528.5	24.6	488	2	O6TQF8
38	528.5	24.6	488	2	AAQ93804
39	528.5	24.6	725	2	Q7RSF6
40	527.5	24.5	465	2	Q8LFC1
41	526	24.5	680	1	YPK1_YEAST
42	524.5	24.4	352	2	Q25115
43	524.5	24.4	648	2	Q9TXB8
44	523.5	24.3	522	2	Q9Y777
45	521.5	24.2	352	1	KAPC_DROME

ALIGNMENTS

RESULT 1

ID	QB6GW6	PRELIMINARY;	PRT;	398 AA.
AC	QB6GW6;			
DT	01-MAR-2003 (Tremblrel. 23, Created)			
DT	01-MAR-2003 (Tremblrel. 23, Last sequence update)			
DT	05-JUL-2004 (Tremblrel. 27, Last annotation update)			
DE	Mus musculus 16 days neonate cerebellum cDNA, RIKEN full-length			
DE	enriched library, clone:9630050F05 product:SIMILAR TO SERINE THREONINE			
DE	KINASE 32 homolog (Mus musculus 7 days neonate cerebellum cDNA, RIKEN			
DE	full-length enriched library, clone:A730009C22 product:SIMILAR TO			
DE	SERINE THREONINE KINASE 32 homolog (Mus musculus adult retina cDNA,			
DE	RIKEN full-length enriched library, clone:A930015B13 product:SIMILAR			
DE	TO SERINE THREONINE KINASE 32 homolog)			
GN	Name=A930015B13Rik;			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Cerebellum, and Retina;			
RC	MEDLINE=99279253; PubMed=10349636;			
RA	Carninci P., Hayashizaki Y.;			
RT	"High-efficiency full-length cDNA cloning.";			
RL	Meth. Enzymol. 303:19-44(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Cerebellum, and Retina;			
RC	MEDLINE=21085660; PubMed=11217851;			
RA	RIKEN FANTOM Consortium;			
RT	"Functional annotation of a full-length mouse cDNA collection.";			
RL	Nature 409:685-690(2001).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Cerebellum, and Retina;			
RA	The FANTOM Consortium,			
RT	the RIKEN Genome Exploration Research Group Phase I & II Team;			
RT	"Analysis of the mouse transcriptome based on functional annotation of			
RT	60,770 full-length cDNAs.";			
RL	Nature 420:563-573(2002).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Cerebellum, and Retina;			
RC	MEDLINE=20493374; PubMed=11042159;			
RA	Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,			
RA	Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;			
RT	"Normalization and subtraction of cap-trapper-selected cDNAs to			
RT	prepare full-length cDNA libraries for rapid discovery of new genes.";			
RL	Genome Res. 10:1617-1630(2000).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Cerebellum, and Retina;			
RC	MEDLINE=20530913; PubMed=11076861;			

RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
RA Yoneda Y., Ishikawa T., Ozawa Y., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Retina;
RA Adachi J., Aizawa K., Hanamura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Anemaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirokawa T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa T., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai K., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akai H., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AK036266; BAC29366.1; -
DR EMBL; AK042599; BAC31302.1; -
DR EMBL; AK044474; BAC31941.1; -
DR HSP; F31751; IGZK.
DR MGD; MG1:2442403; A930015B13R1K.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000961; Pkinase C.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser Thr kinase.
DR InterPro; IPR008271; Ser Thr_pkin_AS.
DR Pfam; PF00069; Pkinase; I.
DR Pfam; PF00433; Pkinase C; 1.
DR ProDom; PD000001; Prot kinase; 1.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 398 AA; 46509 MW; 689BCA5B25CF18BB CRC64;

Query Match 87.4%; Score 1880; DB 2; Length 398;
Best Local Similarity 91.2%; Pred. No. 9e-118;
Matches 351; Conservative 20; Mismatches 14; Indels 0; Gaps 0;

QY 1 MGANTSRKPPVDEENVDNFHFEILRAIGKSGFKVCIVQKNDPKYAMKYNKQKV 60
DB EMBL; AK036266; BAC29366.1; -
QY 1 MGANTSSKAPVDEENVDNFHFEILRAIGKSGFKVCIVRKNPKYAMKYNKQKV 60
DB EMBL; AK042599; BAC31302.1; -
QY 61 ERNEVRNVFKELQIQMGLEHPLVNLVYFQDEDMFVVDLLGGDLRYHLQNVHFE 120
DB EMBL; AK044474; BAC31941.1; -
QY 61 ERNEVRNVFKELQIQMGLEHPLVNLVYFQDEDMFVVDLLGGDLRYHLQNVHFE 120
DB EMBL; AK042599; BAC31302.1; -
QY 121 ETVKLFICELVVALDYLNQRIIHRDMKPDNILLDEGHVHITDFNIAAMLPRETQITM 180
DB EMBL; AK042599; BAC31302.1; -
QY 121 DTVKLFICELVVALDYLNQRIIHRDMKPDNILLDEGHVHITDFNIAAMLPKETRIIV 180
DB EMBL; AK042599; BAC31302.1; -
QY 181 AGTKPYMAPFSSRKAGYSPVDMWSLGVTVAYELLGRPRYHRSSTSSKEIVHVFET 240
DB EMBL; AK042599; BAC31302.1; -
QY 181 AGTKPYMAPFSSRKAGYSPVDMWSLGVTVAYELLGRPRYHRSSTSSKEIVHVFET 240
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QY 241 TVVTPYSAWSQBMVSKLLKLEPNPQRFQSLSDVQNPYNDINWDVAFQKRLPGIP 300
DB EMBL; AK042599; BAC31302.1; -
QY 241 AIVTPYSAWSQBMVSKLLKLEPNPQRFQSLSDVQNPYNDINWDVAFQKRLPGIP 300
DB EMBL; AK042599; BAC31302.1; -

QY 301 NKGRNLCDPTFELEEMILESKPLHKKKRLAKKEKMKRCDSSQTCILQHLDSVQKEFI 360
DB EMBL; AK042599; BAC31302.1; -
QY 301 TKGRNLCDPTFELEEMILESKPLHKKKRLAKKEKMKRCDSSQTCILQHLDAVQKEFI 360
DB EMBL; AK042599; BAC31302.1; -
QY 361 IFNREKYNRDPNFKQPNLALEQTKN 385
DB EMBL; AK042599; BAC31302.1; -
QY 361 IFNREKYNRDPNFKQPNLALEQTKN 385
DB EMBL; AK042599; BAC31302.1; -

RESULT 2

Q7TPQ4 PRELIMINARY; PRT; 368 AA.
AC Q7TPQ4
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE A930015B13R1K protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Olfactory epithelium;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Olfactory epithelium;
RA Strausberg R.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; BC055002; AAH55002.1; -
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein-serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000961; Pkinase C.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008271; Ser Thr_pkin_AS.
DR Pfam; PF00069; Pkinase; I.
DR Pfam; PF00433; Pkinase C; 1.
DR ProDom; PD000001; Prot kinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 368 AA; 43213 MW; 0DE7F6977C39BB56 CRC64;

Query Match

79.4%; Score 1707; DB 2; Length 368;

Best Local Similarity 84.2%; Pred. No. 3.1e-106;

Matches 324; Conservative 17; Mismatches 14; Indels 30; Gaps 1;

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Qy 1 MGANTSRRKPPVFDENEDVNFDPHFELRAIGKSGFGKVCIVQKNDTKKMYAMKYNKQKCV 60
Db 1 MGANTSSKAPVFDENEDVNFDPHFELRAIGKSGFGKVCIVQKNDTKKMYAMKYNKQKCV 60
Qy 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDFMFVVDLLGGDLRYHLQNVHPKE 120
Db 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDFMFVVDLLGGDLRYHLQNVHPKE 120
Qy 121 ETVKLFCELVMAIDYLNQRIIHRDKMKNILLDEHGHVHTDFNTAAMPRETQITTM 180
Db 121 DTVKLFCELVMAIDYLNQRIIHRDKMKNILLDEHGHVHTDFNTAAMPRETQITTM 180
Qy 181 AGTKPYMAPFSSKAGYSFAVDWWSLGVATYELLGRPPYHRSSTSSKEIVHTPET 240
Db 181 AGTKPYMAPFSSKAGYSFAVDWWSLGVATYELLGRPPYHRSSTSSKEIVHTPET 240
Qy 241 TVVTYPSAWSQEMVSLKLLKLEPNPDQFSLSDVQNFPPYMNIDINWDAVFKRLIPGIP 300
Db 241 TVVTYPSAWSQEMVSLKLLKLEPNPDQFSLSDVQNFPPYMNIDINWDAVFKRLIPGIP 300
Qy 301 NGRLNCDPTFELBEEMILESKPLHKKKRLAKKEDMKRCDSSQTCLLQEHLDVQKEFI 360
Db 301 NGRLNCDPTFELBEEMILESKPLHKKKRLAKKEDMKRCDSSQTCLLQEHLDVQKEFI 360
Qy 361 IFNREKVRNDRFNKQPNLALEQTKD 385
Db 361 IFNREKVRNDRFNKQPNLALEQTKD 385
Qy 331 IFNREKVRNDRFNKQPNLALEQTKN 355
Db 331 IFNREKVRNDRFNKQPNLALEQTKN 355

RESULT 3
Q6Q72 ID Q6Q72 PRELIMINARY; PRT; 396 AA.
AC Q6Q72;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haeh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.H.,
Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Kryzyski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus

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initiative."
RT Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RA Klein S., Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; BC072876; AAH72876.1; -.
DR InterPro; IPR011009; Kinase-like.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser Thr kinase.
DR InterPro; IPR008271; Ser Thr_kin_AS.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Hypothetical protein; Kinase;
SQ Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 396 AA; 45626 MW; 991810CE21523F85 CRC64;

Query Match 71.08; Score 1527; DB 2; Length 396;
Best Local Similarity 75.4%; Pred. No. 3.8e-94;
Matches 288; Conservative 41; Mismatches 47; Indels 6; Gaps 2;

Qy 1 MGANTSRRKPPVFDENEDVNFDPHFELRAIGKSGFGKVCIVQKNDTKKMYAMKYNKQKCV 60
Db 1 MGANTSSKAPVFDENEDVNFDPHFELRAIGKSGFGKVCIVQKNDTKKMYAMKYNKQKCV 60
Qy 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDFMFVVDLLGGDLRYHLQNVHPKE 120
Db 61 ERNEVRNVFKELQIMQGLEHPFLVNLWYSFQDEEDFMFVVDLLGGDLRYHLQNVHPKE 120
Qy 121 ETVKLFCELVMAIDYLNQRIIHRDKMKNILLDEHGHVHTDFNTAAMPRETQITTM 180
Db 121 ASVKLYICELALADYLNQSIHRDKMKNILLDEHGHVHTDFNTAAMPRETQITTM 180
Qy 181 AGTKPYMAPFSSKAGYSFAVDWWSLGVATYELLGRPPYHRSSTSSKEIVHTPET 240
Db 181 AGTKPYMAPFSSKAGYSFAVDWWSLGVATYELLGRPPYHRSSTSSKEIVHTPET 240
Qy 241 TVVTYPSAWSQEMVSLKLLKLEPNPDQFSLSDVQNFPPYMNIDINWDAVFKRLIPGIP 300
Db 241 ATVTYPSAWSQEMVSLKLLKLEPNPDQFSLSDVQNFPPYMNIDINWDAVFKRLIPGIP 300
Qy 301 NGRLNCDPTFELBEEMILESKPLHKKKRLAKKEDMKRCDSSQTCLLQEHLDVQKEFI 360
Db 301 TGRLNCDPTFELBEEMILESKPLHKKKRLAKKEDMKRCDSSQTCLLQEHLDVQKEFI 360
Qy 361 IFNREKVRNDRFNKQPNLALEQ 382
Db 361 VFNREK---SYSKQ---LAVHQ 376

RESULT 4
Q9JUX8 ID Q9JUX8 PRELIMINARY; PRT; 414 AA.
AC Q9JUX8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 25, Last annotation update)
DE Serine/threonine protein kinase.
GN Name=Stk32;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

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Tue Dec 21 14:31:35 2004

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RC TISSUE=Brain cDNA;
RX MEDLINE=20164328; PubMed=10700184;
RA Ruiz-Perez V.L., Ide S.E., Strom T.M., Lorenz B., Wilson D., Woods K.,
RA King L., Francamano C., Freisinger P., Spranger S., Marino B.,
RA Dallapiccola B., Wright M., Meitinger T., Polymetopoulos M.H.,
RA Goodship J.;
RT "Mutations in a new gene in Ellis-van Creveld syndrome and Weyers
RT acrocentric dysostosis.";
RL Nat. Genet. 24:283-286(2000).
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AJ250840; CAB76566.1; --
DR HSP; P31751; 1GZK
DR MGD; MGI:192552; Sck32.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR008271; Ser_thr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 414 AA; 47917 MW; BE394415790B9A13 CRC64;

Query Match 67.0%; Score 1441; DB 2; Length 414;
Best Local Similarity 68.3%; Pred. No. 2.3e-88;
Matches 280; Conservative 43; Mismatches 71; Indels 16; Gaps 4;

QY 1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFKVCIQKNDTKKMYAMKYNKQKCV 60
Db 1 MGNHSHKPPVFDENEVNFDFHQLRAIGKSGFKVCIVQKRDTKKMYAMKYNKQKCV 60

QY 61 ERNEVRNVFKELQIQGLEHPLVNLWYSFQDEDMFVVDLLGGDLRYHLQNVHPKE 120
Db 61 ERDEVNRNVFRELQIQGLEHPLVNLWYSFQDEDMFVVDLLGGDLRYHLQNVHTE 120

QY 121 ETVKLFICELVMDLYQNRIIHRDKPDNLLDEHGHVHTIDFNIAAMLPRETOITM 180
Db 121 ETVKLFICELVMDLYQNRIIHRDKPDNLLDEHGHVHTIDFNIAAMLPRETOITM 180

QY 181 AGTKPYMAPEMFS--SRKAGYSFAVDWWSLGVYAYELLGRPPHYTHRSSTSSKEIVHTF 238
Db 181 AGTKPYMAPEVFQVYVDDGGYSYPVDWWSLGVYAYELLGRWRPYEIHSAITPIDILNMF 240

QY 239 EITVTYTPSAWQWYSLKLLKLEPNPDQRFQSLSDVQNFPMYNDINWDVAFQKRLIPGF 298
Db 241 KVERVHYSWCWGWWSLKLKLTQDPESRLSLRDIQSMVYLDNWDVAFKALMPGF 300

QY 299 IPNKGRLNCDPTFELEEMILESKPLHKKKRLAK-KEKDMRKDSSQTCLEHLDVQK 357
Db 301 VPKNGRLNCDPTFELEEMILESKPLHKKKRLAKHRSRSTKDSCLPLNGHLQCCLETVRK 360

QY 358 EFTIFNREKVRNDFNKPQNLALQYKDPQVT--NQMDTGLSETPQTSK 405
Db 361 EFTIFNREKLR-----QQHGDQLSLDGRIGSQTSKSLQDGR 399

RESULT 5
Q7TMD3 PRELIMINARY; PRT; 414 AA.
AC Q7TMD3;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Serine/threonine kinase 32b.
GN Name=Stk32b;
OS Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Brain, and Mouse;
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Lomellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzyszewski M.I., Skalska U., Smailus D.B., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Mouse;
Strausberg R.;
Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
[3]
SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Mouse;
Strausberg R.;
Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
[4]
SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Brain;
Strausberg R.;
Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
-1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
EMBL; BC052404; AAH52404.1; --
EMBL; BC058412; AAH58412.1; --
EMBL; BC056396; AAH56396.1; --
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
InterPro; IPR000719; Prot kinase.
InterPro; IPR008271; Ser_thr_pkinase.
Pfam; PF00069; Pkinase; 1.
ProDom; PD000001; Prot kinase; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 414 AA; 47916 MW; 3C394415790594F3 CRC64;

Query Match 66.9%; Score 1438.5; DB 2; Length 414;
Best Local Similarity 70.2%; Pred. No. 3.3e-88;
Matches 278; Conservative 36; Mismatches 63; Indels 19; Gaps 3;

QY 1 MGANTSRKPPVFDENEDVNFDFEILRAIGKSGFKVCIQKNDTKKMYAMKYNKQKCV 60
Db 1 MGNHSHKPPVFDENEVNFDFHQLRAIGKSGFKVCIVQKRDTKKMYAMKYNKQKCV 60

QY 61 ERNEVRNVFKELQIQGLEHPLVNLWYSFQDEDMFVVDLLGGDLRYHLQNVHPKE 120
Db 61 ERDEVNRNVFRELQIQGLEHPLVNLWYSFQDEDMFVVDLLGGDLRYHLQNVHTE 120

QY 121 ETVKLFICELVMDLYQNRIIHRDKPDNLLDEHGHVHTIDFNIAAMLPRETOITM 180
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Db 121 GTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEGHVHITDFNIATVLKSGSEKASSM 180
Qy 181 AGTKPYMAPEWFS--SRKGAGYSFADVWWSLGVTAAYELLRRRYPYHRSSTSSKEIVHTF 238
Db 181 AGTKPYMAPEVQVYVDDGGPGYSYPVDWWSLGVTAAYELLRRGRWREYEHSAIPIDEILNMF 240
Qy 239 ETTVVTVTPSAWSQEWMSLLKLLPNPDQRFSQLSDVQNPYPYMDINWDAVFOKRLIPGF 298
Db 241 KVERVHYSSTWCGWWSLLKLLTKDPESRUSSURDIQSMYTLADMWDAVFEKALMPGF 300
Qy 299 IPNKGRLNCDPTFELEEMILESPLHKKKKELAK-KEKDMKCKDSSQTCILQEHLDVQK 357
Db 301 VPKNGRLNCDPTFELEEMILESPLHKKKKELAKHRSRDSSTKDCSPLNGHLQOCLETVRK 360

RESULT 6
AAH58412
ID AAH58412 PRELIMINARY; PRT; 414 AA.
AC AAH58412;
DT 24-MAY-2004 (TrEMBLrel. 27, Created)
DT 24-MAY-2004 (TrEMBLrel. 27, Last sequence update)
DT 24-MAY-2004 (TrEMBLrel. 27, Last annotation update)
DE Serine/threonine kinase 32B.
GN STK32B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Mouse;
RX MEDLINE=22388257; PubMed=12477932;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinstead J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Mouse;
RX Strauberg R.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC058412; AAH58412.1; -.
KW Kinase.
SQ SEQUENCE 414 AA; 47916 MW; 3C3944415790594F3 CRC64;

Query Match 66.9%; Score 1438.5; DB 2; Length 414;
Best Local Similarity 70.2%; Pred. No. 3.3e-88;
Matches 278; Conservative 36; Mismatches 63; Indels 19; Gaps 3;

Qy 1 MGATSRKPPVFDENEDVNFHETLRAIGKSGFGKVCIVOKNTDKYAMKYNKOKCV 60
Db 1 MGNHSHKPPVFDENEENVDHFDQLRAIGKSGFGKVCIVOKNRDITKGMAMKYNKOKCV 60
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Qy 61 ERNEVRNVFKELOIMQGLEHPFLVNLWYSFQDEDMFWVDLLGGDLRYHLQONVHPKE 120
Db 61 ERNEVRNVFKELOIMQGLEHPFLVNLWYSFQDEDMFWVDLLGGDLRYHLQONVHPTE 120
Qy 121 ETVKLFICELVMDYLNQRIIHRDMKPDNILLDEGHVHITDFNIATVLKSGSEKASSM 180
Db 121 GTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEGHVHITDFNIATVLKSGSEKASSM 180
Qy 181 AGTKPYMAPEWFS--SRKGAGYSFADVWWSLGVTAAYELLRRRYPYHRSSTSSKEIVHTF 238
Db 181 AGTKPYMAPEVQVYVDDGGPGYSYPVDWWSLGVTAAYELLRRGRWREYEHSAIPIDEILNMF 240
Qy 239 ETTVVTVTPSAWSQEWMSLLKLLPNPDQRFSQLSDVQNPYPYMDINWDAVFOKRLIPGF 298
Db 241 KVERVHYSSTWCGWWSLLKLLTKDPESRUSSURDIQSMYTLADMWDAVFEKALMPGF 300
Qy 299 IPNKGRLNCDPTFELEEMILESPLHKKKKELAK-KEKDMKCKDSSQTCILQEHLDVQK 357
Db 301 VPKNGRLNCDPTFELEEMILESPLHKKKKELAKHRSRDSSTKDCSPLNGHLQOCLETVRK 360

RESULT 7
Q8C4E0
ID Q8C4E0 PRELIMINARY; PRT; 414 AA.
AC Q8C4E0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 0 day neonate cerebellum cDNA, RIKEN full-length enriched
DE library, clone:C230053G02 product:serine threonine kinase 32, full
DE insert sequence.
GN Name=Stk32;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
[4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=20493374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
[5]
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RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; Tissue=Cerebellum;
RX MEDLINE=20530913; PubMed=11076861;
RA Kono H., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
RA Shibata K., Itoh M., Aizawa K., Kitano T., Tashiro H., Itoh M.,
RA Kono H., Akiyama J., Nishi K., Kitano T., Nishine T., Harada A.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; Tissue=Cerebellum;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AK082468; BAC38500.1; -.
DR HSP; P31751; IGZK.
DR MGD; MGI:1927552; Sck32.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; E:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser Thr_kinase.
DR InterPro; IPR008271; Ser_thr_kinase_AS.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 414 AA; 47884 MW; 9C394364BE19E945 CRC64;

Query Match 66.7%; Score 1434.5; DB 2; Length 414;
Best Local Similarity 69.9%; Pred. No. 6.2e-88;
Matches 277; Conservative 37; Mismatches 63; Indels 19; Gaps 3;

QY 1 MGNTSRKPPVFDNEVDNFDHFEILRAIGKSGFGKVCIVQKNDTKQYAMKYNKQKCV 60
DB 1 MGNHSHKPPVFDNEVDNFDHFEILRAIGKSGFGKVCIVQKNDTKQYAMKYNKQKCV 60
QY 61 ERNEVRNVFKELOIMQGLHEHPFLNVLWYSFQDEDMFVVDLLGGDLRYHLQNVHPKE 120
DB 61 ERDEVRNVFRELQIMQGLHEHPFLNVLWYSFQDEDMFVVDLLGGDLRYHLQNVHPKE 120
QY 121 ETVKLFICELVMDLYLQNRQIHRDKPDNILLDEGHVHITDFNIAAMLPRETQITTM 180
DB 121 GTVKLYICELALALEYLQRYHIHRDKPDNILLDEGHVHITDFNIAATLVKSEKASSV 180
QY 181 AGTKPYMAPEMFS--SRKAGYSFAVDWWSLGVTAAYELLRGRPPYHRSSTSSKEIVHTF 238
DB 181 AGTKPYMAPEVQVYVDGPGYSYFVDWWSLGVTAAYELLRGRPPYHRSATPIDEILNMF 240
QY 239 ETTVVTYPSANQSEWVSLKLLLEPNPDQPSQLSDVQNFPPYMDINWDVFKRLIPGF 298
DB 241 KVERVHYSSTWCEGWSVSLKLLTKDPELSRLSSLRDIQSMYLDAMNDWVFKALMPGF 300

QY 299 IPNKGRLNCPTFELEEMILESPLHKKKRLAK-KEKDMRKCDSSQTCILQEHLDVOK 357
DB 301 VPKNGRLNCPTFELEEMILESPLHKKKRLAKRSDTKDSCPLNGHLQOCLETYRK 360
QY 358 EFILFNEKVNDRDNKQPNLALQTKDPPQVINGQM 393
DB 361 EFILFNEKURRQ-----QHNQQL 380

RESULT 8
Q9NY57 PRELIMINARY; PRT; 414 AA.
ID Q9NY57
AC Q9NY57;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Serine/threonine protein kinase.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole brain cDNA;
RX MEDLINE=20164328; PubMed=10700184;
RA Ruiz-Perez V.L., Ide S.E., Strom T.M., Lorenz B., Wilson D., Woods K.,
RA King L., Francmano C., Freisinger P., Spranger S., Marino B.,
RA Dallapiccola B., Wright M., Meitinger T., Polymetopoulos M.H.,
RA Goodship J.;
RT "Mutations in a new gene in Ellis-van Creveld syndrome and Weyers
RT acrodermatol dysostosis";
RL Nat. Genet. 24:283-286(2000).
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AJ250839; CAB76471.1; -.
DR HSP; P31751; IGZK.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; E:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008271; Ser_thr_kinase_AS.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 414 AA; 47883 MW; 8FCD58A67E909B0E CRC64;

Query Match 66.2%; Score 1423.5; DB 2; Length 414;
Best Local Similarity 72.3%; Pred. No. 3.4e-87;
Matches 269; Conservative 40; Mismatches 60; Indels 3; Gaps 2;

QY 1 MGNTSRKPPVFDNEVDNFDHFEILRAIGKSGFGKVCIVQKNDTKQYAMKYNKQKCV 60
DB 1 MGNHSHKPPVFDNEVDNFDHFEILRAIGKSGFGKVCIVQKNDTKQYAMKYNKQKCV 60
QY 61 ERNEVRNVFKELOIMQGLHEHPFLNVLWYSFQDEDMFVVDLLGGDLRYHLQNVHPKE 120
DB 61 ERDEVRNVFRELQIMQGLHEHPFLNVLWYSFQDEDMFVVDLLGGDLRYHLQNVHPKE 120
QY 121 ETVKLFICELVMDLYLQNRQIHRDKPDNILLDEGHVHITDFNIAAMLPRETQITTM 180
DB 121 GTVKLYICELALALEYLQRYHIHRDKPDNILLDEGHVHITDFNIAATLVKGAERASSM 180
QY 181 AGTKPYMAPEMFS--SRKAGYSFAVDWWSLGVTAAYELLRGRPPYHRSSTSSKEIVHTF 238
DB 181 AGTKPYMAPEVQVYVDGPGYSYFVDWWSLGVTAAYELLRGRPPYHRSATPIDEILNMF 240
QY 239 ETTVVTYPSANQSEWVSLKLLLEPNPDQPSQLSDVQNFPPYMDINWDVFKRLIPGF 298
DB 241 KVERVHYSSTWCKGWSVSLKLLTKDPELSRSLSSLRDIQSVFYLDAMNDWVFKALMPGF 300

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RL Genome Res. 13:2265-2270(2003).
CC -I- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AY358353; AAQ88719.1; -.
DR InterPro; IPR011009; Kinase-like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_kin_AS.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TK; 1.
DR SMART; SM00219; TyRK; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00108; Serine/threonine-protein kinase; Transferase.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 364 AA; 42195 MW; F552D0CB54C7A27C CRC64;

Query Match 55.2%; Score 1186.5; DB 2; Length 364;
Best Local Similarity 69.9%; Pred. No. 2.1e-71;
Matches 225; Conservative 38; Mismatches 56; Indels 3; Gaps 2;

QY 51 MKYMKKQKVERNEVRNFKELQIMQGLEHPLVNLWYSFQDEEDMFVVDLLGGDLRY 110
DB 1 MKYMKKQKCIERDEVNRNFKELQIMQGLEHPLVNLWYSFQDEEDMFVVDLLGGDLRY 60

QY 111 HLQONVHFEETVKLFICELVMALDYLNQRIIHRDKPDNILLDEGHVHITDFNIAAM 170
DB 61 HLQONVHFEETVKLFICELALALEYLQRYHIIHRDKPDNILLDEGHVHITDFNIAATV 120

QY 171 LPRETQITTMAGTKPYMAPEMPS--SRKGAGYSFVADWMSLGVTAAYELLGRPPYHRS 228
DB 121 VKGAERASSMAGTKPYMAPEVFQVYMDRPGYSGYFVDMWSLGITAYELLGRWPRPYEHSV 180

QY 229 TSKEIIVHTFTVTVTYPSAQMVSLLKLEPNPDRFSQSDVQNFPMYNDINWDA 288
DB 181 TPDEILNMFKVERVHYSTWCKGMVALLKLLTKDPESRVSSLDHIOQSVPLADMWDA 240

QY 289 VFQKRLIPGIPNKGRLNCDPTFEELMILESKPLHKKKKRLAK-KEKDMRKCDSSQTCL 347
DB 241 VFKKALMPGFVNPNGRLNCDPTFEELMILESKPLHKKKKRLAKNRSDGTKDCSPLNGH 300

QY 348 LOEHLDSVQKEFIIFNREKNR 369
DB 301 LQHCLETVREEFIFNREKLRR 322

RESULT 15
Q86UE1 PRELIMINARY; PRT; 369 AA.
ID Q86UE1
AC Q86UE1; 2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2004 (TrEMBLrel. 26, Last annotation update)
DE PKE protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=2238257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshitoki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahay J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.B., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
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Strausberg R.;
RA Submitted (JAN-2003) to the EMBL/GenBank/DBDJ databases.
CC -i- SIMILARITY: Belongs to the Ser/thr protein kinase family.
DR EMBL; BC045760; AAH45760.1; -.
DR HSSP; O15530; 1H1W.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 369 AA; 42395 MW; E152C66BB2D786B4 CRC64;

Query Match 53.1%; Score 1142; DB 2; Length 369;
Best Local Similarity 63.2%; Pred. No. 2e-68;
Matches 216; Conservative 50; Mismatches 72; Indels 4; Gaps 2;

Qy 48 MYAMKYNKQKQVERNEVNFKEIQMGLEHPFLVNLWYSFQDEEDMFVVDLLCGD 107
Db 1 MYAMKYNKQKQIERDEVNFVRELEILQEHVFLVNLWYSFQDEEDMFVVDLLCGD 60

Qy 108 LRYHLQNVHPKEBTVKLFICELVNLQYQRIIHRDMKPDNILLDEGHVHTDFNI 167
Db 61 LRYHLQNVQPSQEDTVRLYICEMALDYLRGQHIHRDVKPDNILLDERGHAHTDFNI 120

Qy 168 AAMLPRETOITTMAGTKPYMAPEMPSS--RYGAGYSFVADWWSLGVTAPELLRGRPYHI 225
Db 121 ATIIKGERATALAGTKPYMAPEIFHSFVNGGTGYSPFVDWWSVGVWAYELLRGWRPYDI 180

Qy 226 RSSTSKEIVHTFTTVVTPSAQSOEMVSLKKLLEPNPDRFQSDVQNFVPMNDIN 285
Db 181 HSSNAVSLVQLFSTVSQYVPTWSKENVALLRKLAVNPEHRLSSLDQVQAAPALAGVL 240

Qy 286 WDAVFQKRLIPGFIPNKGRLNCDPTFELEEMILESKPLHKKKKGLAKKEDMRKCDSSQT 345
Db 241 WDLSEKRVPEPGFVFNKGRGLHCDPTFELEEMILESRPLHKKKKGLAKNKSQSDNSRDSQS 300

Qy 346 --CLLOEHLDSVQKEFIIFNREKVNDRDNKQPNLALQTKD 385
Db 301 ENDYLODCLDAIQODFVIFNREKLKRSQDLPREPLPAPESRD 342

Search completed: December 17, 2004, 09:26:44
Job time : 78 secs

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